

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 10:21:42 ; Search time 310.82 seconds  
(without alignments)  
5.481 Million cell updates/sec

Title: US-09-763-397A-6  
Perfect score: 127  
Sequence: 1 KPKDELVDENDIKKICKMEKCS 23

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A.Geneseq\_1101.\*  
1: /SID8/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID8/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID8/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID8/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID8/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID8/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SID8/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SID8/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SID8/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID8/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SID8/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SID8/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SID8/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SID8/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SID8/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SID8/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SID8/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SID8/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID8/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID8/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID8/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID8/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	100.0	23	21	AAV70282
2	127	100.0	66	16	AA66442
3	127	100.0	309	11	AA13175
4	127	100.0	319	11	AA607945
5	127	100.0	319	12	AA13176
6	127	100.0	327	12	AA13177
7	127	100.0	335	12	AA13178
8	127	100.0	335	12	AA13179
9	127	100.0	350	21	AAV70278
10	127	100.0	411	9	AA68314
11	127	100.0	412	7	AA60416

12	127	100.0	424	14	AA37796
13	123	96.9	412	9	AA680835
14	121	95.3	424	14	AA37797
15	120	94.5	180	11	AA607290
16	96	75.6	40	16	AA687213
17	75	59.1	20	16	AA671651
18	71	55.9	21	21	AAV70283
19	62	48.8	14	16	AA671655
20	62	48.8	19	7	AA61002
21	60.5	47.6	402	8	AA670709
22	58.5	46.1	19	16	AA671654
23	58.5	46.1	168	11	AA607291
24	58.5	46.1	272	10	AA693560
25	56.5	44.5	478	21	AA607288
26	53	41.7	19	21	AAV99033
27	53	41.7	20	22	AAJ04118
28	53	41.7	21	10	AA691504
29	53	41.7	21	16	AA682586
30	53	41.7	21	16	AA678920
31	53	41.7	21	16	AA675955
32	53	41.7	21	16	AA670912
33	53	41.7	21	17	AA605612
34	53	41.7	21	18	AA635440
35	53	41.7	21	20	AAV23252
36	53	41.7	21	21	AAV80071
37	53	41.7	21	21	AAV54553
38	53	41.7	21	21	AAV58777
39	53	41.7	21	22	AA699706
40	53	41.7	21	22	AA662428
41	53	41.7	21	22	AA684517
42	53	41.7	21	22	AA688269
43	53	41.7	21	22	AA689366
44	53	41.7	21	22	AA684447
45	53	41.7	21	22	AA698457

#### ALIGNMENTS

RESULT 1  
ID AAV70282 standard; peptide; 23 AA.  
AAV70282;  
AC AAV70282;  
XX  
DT 06-JUN-2000 (first entry)  
XX  
DE Plasmodium falciparum CSP antigenic epitope, p593.  
XX  
KW Recombinant protein; CDC/NITMVA-1; multivalent; malaria; vaccine;  
KW T-cell epitope; tetanus toxoid; antigenic epitope; treatment;  
KW Circumsporozoite protein; CSP; sporozoite surface protein-1; MSP-2;  
KW liver stage antigen-1; USA-1; merozoite surface protein-1; MSP-1;  
KW apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175;  
KW EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen;  
KW Pf27; antiparasitic; prevention; anti-CDC/NITMVA-1 antibody.  
XX  
OS Plasmodium falciparum.  
XX  
PN WO20001179-A1.  
XX  
PD 02-MAR-2000.  
XX  
PF 19-AUG-1999; 99MO-US18869.  
XX  
PR 21-AUG-1998; 98US-0097703.  
XX  
PA (NAIM-) NAT INST IMMUNOLOGY.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Lal AA, Shi YP, Hasnain SE;  
XX  
DR WPI; 2000-237654/20.

RIS protein. Syn  
Sequence encoded b  
RIS\* protein. Syn  
Circumsporozoite a  
P. falciparum deriv  
CS Region II\* mme  
Plasmodium falcipa  
Circumsporozoite a  
Sequence corresp.  
Plasmodium cynomol  
CS Region II\* mme  
Circumsporozoite a  
Plasmodium berghei  
Human IL-2/ P. yoe  
HSA class II bindi  
P. falciparum CS pr  
Sequence of modifi  
Plasmodium falcipa  
Malaria circumspor  
P. falciparum CS p  
Malaria circumspor  
Circumsporozoite h  
T-cell stimulatory  
Peptide derived fr  
Pathogen derived T  
T helper cell (Th)  
Unidentified pepti  
Plasmodium falcipa  
Plasmodium falcipa  
Plasmodium falcipa  
Plasmodium falcipa  
Sequence of T help  
Plasmodium falcipa

XX Novel recombinant protein as vaccine for treating malarial infection  
 PT comprises antigenic peptides obtained from different stages of  
 PT Plasmodium falciparum life cycle  
 PS Claim 2; Page 16; 52pp; English.  
 CC The present sequence is the antigenic epitope P593, derived from  
 CC circumsporozoite protein (CSP) of the sporozoite stage of Plasmodium  
 CC falciparum. It is used in the construction of recombinant protein  
 CC CDC/NITMAYAC-1, which is a multivalent, multistage malarial vaccine.  
 CC The recombinant protein comprises, melittin signal peptide, (His)6 tag,  
 CC T-cell epitope from tetanus toxoid and 21 antigenic epitopes from  
 CC circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2),  
 CC liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1),  
 CC (EBA-175), rhoptry associated protein-1 (RAP-1), erythrocyte binding antigen-175  
 CC antigen, Pfgr27. These epitopes were obtained at different stages of the  
 CC life cycle of P. falciparum. CDC/NITMAYAC-1 vaccine has antiparasitic  
 CC activity and can be used for treatment and prevention of malarial  
 CC infections. Anti-CDC/NITMAYAC-1 antibodies can be used for detecting  
 CC P. falciparum in biological samples.  
 SO Sequence 23 AA;

Query Match 100.0%; Score 127; DB 21; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 8, 4e-12;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPKDELVDYNDIEKKICKMEKCS 23  
 1 kpkdelvyndiekkickmekcs 23

RESULT 2

AAR66442  
 ID AAR66442 standard; peptide; 66 AA.

AC AAR66442;

DT 03-AUG-1995 (first entry)

DE Plasmodium falciparum circumsporozoite antigen.

KM T cell helper site; cytotoxic T cell response; neutralising antibody;  
 KM P. falciparum CS antigen; circumsporozoite; malaria; vaccine.

OS Synthetic.

Key Location/Qualifiers  
 FT Region 22..41  
 FT /label="repeat\_region  
 FT /note="(NANP)5"

PN WO9426785-A.

PD 24-NOV-1994.

PF 13-MAY-1994; 94WO-US05142.

PR 14-MAY-1993; 93US-0060988.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA (USSH ) US SEC DEPT HEALTH.

PI Ahlers JD, Berzofsky JA, Nara P, Pendleton CD, Shirai M;  
 DR WPI; 1995-006707/01.

PT Polypeptide inducing helper T cell, cytotoxic T cell and  
 PT antibodies responses - to target antigen in hosts of different  
 PT MHC haplotypes, esp. for therapeutic or prophylactic vaccines

PT against HIV.

PS Example 4; Page 54; 120pp; English.

CC The peptide AAR66442 was synthesised to make a peptide vaccine which  
 CC is recognised by a broad range of MHC types that will elicit a T  
 CC helper cell response, a CTL response and a high titre neutralising  
 CC antibody response.  
 SO Sequence 66 AA;

Query Match 100.0%; Score 127; DB 16; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 2, 7e-11;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPKDELVDYNDIEKKICKMEKCS 23  
 44 kpkdelvyndiekkickmekcs 66

RESULT 3

AAR13175  
 ID AAR13175 standard; Protein; 309 AA.

AC AAR13175;

DT 29-AUG-1991 (first entry)

DE NS1\_81-RLfdelta9.

KM Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;  
 KM hybrid; influenza virus; non-structural protein 1; fusion.  
 OS Plasmodium falciparum.

OS Influenza virus (A/PR/8/34/).

Key Location/Qualifiers  
 FT Region 1..81  
 FT /label="N-terminal of NS1  
 FT /note="Influenza virus nonstructural protein 1"  
 FT /label="synthetic linker  
 FT 88  
 FT /label="artifact  
 FT /note="see comments"  
 FT 89..193  
 FT /label="AAs 19-123 of CS protein  
 FT /note="Region 1 contg. flanking region less  
 FT 194..309  
 FT /label="AAs 297-412 of CS protein  
 FT /note="Region II flanking region minus 9 N-term-  
 FT inal AAs"

Region

PN EP432965-A.

PD 19-JUN-1991.

PF 06-DEC-1990; 90EP-0313257.

PR 08-DEC-1989; 89US-0447746.

PA (SMIK ) SMITHKLINE BEECHAM.  
 PA (USSA ) US SEC OF THE ARMY.  
 PA (BIOM-) BIOMEDICAL RES INST.

PI Gross MS, Gordon DM, Hollingdale MR;  
 DR WPI; 1991-179771/25.

PT Polypeptide comprising immunogenic determinants from P falciparum  
 PT - for vaccine against malaria infection in humans.

XX Example 1; Page 7; 18pp; English.

PS The polypeptide is prep'd. by genetic engineering of genes encoding  
 CC the P. falciparum circumsporozoite (CS) protein [Deme et al.,  
 CC Science 225 : 593 (1984)], and the influenza virus non-structural  
 CC protein 1 (NS1). [Baez et al., Nucleic Acids Research, 8 : 5845  
 CC (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NS1  
 CC (NS1-81) is linked via a synthetic sequence to DNA encoding Region  
 CC I contg. flanking regionless the 18 AA signal region, which in  
 CC turn is fused to DNA encoding Region II contg. flanking region  
 CC less the first nine N-terminal AAs. This CS fusion is designated  
 CC Rlfelta9. The Pro residue separating the Asp (at the C-terminal  
 CC of the linker) from Rlfelta9 is an artifact of a filled in BamHI  
 CC site. The peptide can be used in a vaccine for protection against  
 CC malaria. See also AAR12306-R12311 and AAR13176-R13179.

CC Sequence 309 AA;  
 SO

Query Match 100.0%; Score 127; DB 12; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPKDELVDYENDIEKKICKMEKCS 23  
 |||  
 Db 265 kpkdelvyendiekkickmekcs 287

RESULT 4  
 AAR07945  
 ID AAR07945 standard; protein; 319 AA.  
 AC AAR07945;  
 XX  
 DT 22-FEB-1991 (first entry)  
 XX  
 DE NS181RLFAuth plasmid product.  
 XX  
 KW Malaria; vaccine.  
 XX  
 OS Plasmodium falciparum.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..81  
 FT /label= NS181 protein fragment  
 FT /note= "from plasmid pmg-1"  
 FT 89..193  
 FT /label= Fragment of circumsporozoite protein  
 FT Domain 204..319  
 FT /label= Fragment of circumsporozoite protein  
 XX  
 EP398540-A.  
 XX  
 PD 22-NOV-1990.  
 XX  
 PF 01-MAY-1990; 90EP-0304720.  
 XX  
 PR 03-MAY-1989; 89US-0346863.  
 XX  
 XX (SMIK ) SMITHKLINE BEECHAM.  
 PA  
 XX Gross MS, Young JF;  
 PI  
 DR WPI; 1990-350299/47.  
 DR N-PSDB; AA006580.  
 XX  
 PT New polypeptide used in malaria vaccine - comprises immunogenic  
 PT determinants from 1st and 2nd flanking regions of plasmodium  
 PT surface protein and intermediate repeat domain  
 XX  
 XX Example 2; Page 11-12; 24pp; English.

XX The product is useful in preparation of vaccines for treatment and  
 CC prophylaxis of plasmodium sporozoite infection. It may be easily  
 CC produced in large pure quantities from a transformed E.coli  
 CC expression system.  
 XX  
 XX Sequence 319 AA;  
 SO

Query Match 100.0%; Score 127; DB 11; Length 319;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-10;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPKDELVDYENDIEKKICKMEKCS 23  
 |||  
 Db 275 kpkdelvyendiekkickmekcs 297

RESULT 5  
 AAR13176  
 ID AAR13176 standard; protein; 319 AA.  
 AC AAR13176;  
 XX  
 DT 29-AUG-1991 (first entry)  
 XX  
 DE NS1-81-RLFAuth.  
 XX  
 KW Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;  
 KW hybrid; Influenza virus; non-structural protein 1; fusion.  
 XX  
 OS Plasmodium falciparum.  
 OS Influenza virus (A/PR/8/34);  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..81  
 FT /label= N-terminal of NS1  
 FT /note= "Influenza virus nonstructural protein 1"  
 FT 82..87  
 FT /label= synthetic linker  
 FT Region 88  
 FT /label= artifact  
 FT /note= "see comments"  
 FT 89..193  
 FT /label= AAs 19-123 of CS protein  
 FT /note= "Region I contg. flanking region less  
 FT signal sequence"  
 FT 194  
 FT /label= artifact  
 FT /note= "see comments"  
 FT 195..319  
 FT /label= AAs 288-412 of CS protein  
 FT /note= "Region II flanking region"  
 XX  
 EP432965-A.  
 XX  
 PD 19-JUN-1991.  
 XX  
 PF 06-DEC-1990; 90EP-0313257.  
 XX  
 PR 08-DEC-1989; 89US-0447746.  
 XX  
 XX (SMIK ) SMITHKLINE BEECHAM.  
 PA (USSA ) US SEC OF THE ARMY.  
 PA (BIOM-) BIOMEDICAL RES INST.  
 XX  
 PI Gross MS, Gordon DM, Hollingdale MR;  
 DR WPI; 1991-179771/25.  
 DR  
 PT Polypeptide comprising immunogenic determinants from P falciparum  
 PT - for vaccine against malaria infection in humans.  
 XX

PS Example 2; Page 10; 18pp; English.

XX The polypeptide is prep'd. by genetic engineering of genes encoding  
 CC the P. falciparum circumsporozoite (CS) protein [Dame et al.,  
 CC Science 225 : 593 (1984)], and the influenza virus non-structural  
 CC protein 1 (NS1), [Baez et al., Nucleic Acids Research, 8 : 5845  
 CC (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NS1  
 CC (NS1\_81) is linked via a synthetic sequence to DNA encoding Region  
 CC I contg. flanking regions less the 18 AA signal region, which in  
 CC turn is fused to DNA encoding Region II contg. flanking region.  
 CC This CS fusion is designated R1Aauth. The Pro residue separating  
 CC the Asp (at the C-terminal of the linker) from R1Aauth is an arti-  
 CC fact of a filled in BamHI site; the Gly separating Region I and  
 CC Region II contg. CS flanking regions is an artifact of a synthetic  
 CC FokI/NotI linker. The peptide can be used in a vaccine for  
 CC protection against malaria.  
 CC The complete nucleotide and AA sequences are given in EP-304720,  
 CC filed May 1, 1990.  
 CC See also AAR12306-R12311 and AAR13175-R13179.

XX Sequence 319 AA;

SO

Query Match 100.0%; Score 127; DB 12; Length 319;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-10;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPKELDYENDIEKKICKMEKCS 23  
 |||||||||||||||||||||

DB 275 kpkeLDYendiekkickmekcs 297

RESULT 6  
 AAR13177  
 ID AAR13177 standard; Protein; 327 AA.

XX AAR13177;  
 AC  
 DT 29-AUG-1991 (first entry)  
 XX  
 DE NS1\_81-R1Aauth + (NANP)2.  
 XX  
 KW Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;  
 KW hybrid; influenza virus; non-structural protein 1; fusion.  
 XX  
 OS Plasmodium falciparum.  
 OS Influenza virus (A/PR/8/34/).

XX Key Location/Qualifiers  
 FH 1..81  
 FT Region  
 FT /label="N-terminal of NS1  
 FT /note="Influenza virus nonstructural protein 1"  
 FT Peptide  
 FT 82..87  
 FT /label="synthetic linker  
 FT Region  
 FT 88  
 FT /label="artifact  
 FT /note="see comments"  
 FT 89..193  
 FT Region  
 FT /label="AAs 19-123 of CS protein  
 FT /note="Region I contg. flanking region less  
 FT signal sequence"  
 FT 194..201  
 FT Region  
 FT /label="immunodominant repeat region  
 FT /note="two tetrapeptide repeat units"  
 FT 202  
 FT Region  
 FT /label="artifact  
 FT /note="see comments"  
 FT 203..327  
 FT Region  
 FT /label="AAs 288-412 of CS protein  
 FT /note="Region II flanking region"  
 XX  
 PN EP432965-A.

PD 19-JUN-1991.

XX  
 PF 06-DEC-1990; 90EP-0313257.  
 XX  
 PR 08-DEC-1989; 89US-0447746.  
 XX  
 PA (SMIR ) SMITHKLINE BEECHAM.  
 PA (USMA ) US SEC OF THE ARMY.  
 PA (BIOM-) BIOMEDICAL RES INST.  
 XX  
 PI Gross MS, Gordon DM, Hollingdale MR;  
 DR WPI; 1991-179771/25.  
 XX  
 PR Polypeptide comprising immunogenic determinants from P falciparum  
 PT - for vaccine against malaria infection in humans.  
 XX

PS Example 3; Page 10; 18pp; English.

XX The polypeptide is prep'd. by genetic engineering of genes encoding  
 CC the P. falciparum circumsporozoite (CS) protein [Dame et al.,  
 CC Science 225 : 593 (1984)], and the influenza virus non-structural  
 CC protein 1 (NS1), [Baez et al., Nucleic Acids Research, 8 : 5845  
 CC (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NS1  
 CC (NS1\_81) is linked via a synthetic sequence to DNA encoding Region  
 CC I contg. flanking region less the 18 AA signal region. This is  
 CC linked to a synthetic sequence encoding two repeat units from the  
 CC immunodominant region, which in turn is fused to DNA encoding the  
 CC Region II contg. flanking region. The Pro residue separating the  
 CC Asp (at the C-terminal of the linker) from the Region I contg. CS  
 CC flanking region is an artifact of a filled-in BamHI site; the Gly  
 CC separating the repeat units and the Region II contg. CS flanking  
 CC region is an artifact of a synthetic FokI/NotI linker. The  
 CC peptide can be used in a vaccine for protection against malaria.  
 CC See also AAR12306-R12311 and AAR13175-R13179.

XX Sequence 327 AA;

SO

Query Match 100.0%; Score 127; DB 12; Length 327;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-10;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPKELDYENDIEKKICKMEKCS 23  
 |||||||||||||||||||||

DB 283 kpkeLDYendiekkickmekcs 305

RESULT 7  
 AAR13178  
 ID AAR13178 standard; Protein; 335 AA.

XX AAR13178;  
 AC  
 DT 29-AUG-1991 (first entry)  
 XX  
 DE NS1\_81(NANP)4R1Aauth.  
 XX  
 KW Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;  
 KW hybrid; influenza virus; non-structural protein 1; fusion.  
 XX  
 OS Plasmodium falciparum.  
 OS Influenza virus (A/PR/8/34/).

XX Key Location/Qualifiers  
 FH 1..81  
 FT Region  
 FT /label="N-terminal of NS1  
 FT /note="Influenza virus nonstructural protein 1"  
 FT 82..97  
 FT Region  
 FT /label="immunodominant repeat region  
 FT /note="four tetrapeptide repeat units"  
 FT 98..103  
 FT Peptide  
 FT /label="synthetic linker



RA Olafsson P., Matile H., Certa U.;  
 RT Plasmodium falciparum: the repetitive MSA-1 surface protein of the  
 RT RO-71 isolate is recognized by mouse antibody against the  
 RT nonrepetitive repeat block of RO-33."  
 RL Exp. Parasitol. 74:381-389(1992).  
 DR EMBL: X61930; CAA43932.1; -  
 DR InterPro: IPR000087; Collagen.  
 FT NON TER 1087  
 SQ SEQUENCE 1087 AA; 123911 MW; 5518852133C01B33 CRC64;

Query Match 57.4%; Score 42.5; DB 5; Length 1087;  
 Best Local Similarity 60.0%; Pred. No. 53;  
 Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 OYKANSKFI-GITE 14  
 ID 09T2T5 PRELIMINARY; PRT; 1694 AA.  
 AC 09T2T5;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE MEROZOITE SURFACE PROTEIN 1 PRECURSOR.  
 GN MSP1.  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5833;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HN1;  
 RA Jiang G., Liu R.Z., Daubenberger C.A., Pluschke G.;  
 RL Submitted (Apr-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF062348; AAC72884.1; -  
 DR InterPro: IPR000561; EGF-like.  
 DR Pfam: PF00008; EGF; 1.  
 KW Merozoite.  
 SQ SEQUENCE 1694 AA; 192794 MW; 84CFC0E709F5673B CRC64;

Query Match 57.4%; Score 42.5; DB 5; Length 1694;  
 Best Local Similarity 60.0%; Pred. No. 84;  
 Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 OYKANSKFI-GITE 14  
 ID 09T2T5 PRELIMINARY; PRT; 1694 AA.  
 AC 09T2T5;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE MAJOR MEROZOITE SURFACE ANTIGEN.  
 GN GP195.  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5833;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FCCL1/HN;  
 RA Shan Z.X., Yu X.B., Li X.R., Ma C.L., Fang J.M.;  
 RT "Molecular cloning and sequence analysis of major merozoite surface  
 RT antigen(gp195)gene of Plasmodium falciparum isolate FCCL1/HN."  
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF218248; AAF37526.1; -

RESULT 14  
 ID 09NHX1 PRELIMINARY; PRT; 1694 AA.  
 AC 09NHX1;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE MAJOR MEROZOITE SURFACE ANTIGEN.  
 GN GP195.  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5833;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FCCL1/HN;  
 RA Shan Z.X., Yu X.B., Li X.R., Ma C.L., Fang J.M.;  
 RT "Molecular cloning and sequence analysis of major merozoite surface  
 RT antigen(gp195)gene of Plasmodium falciparum isolate FCCL1/HN."  
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF218248; AAF37526.1; -

DR InterPro: IPR000561; EGF-like.  
 DR Pfam: PF00008; EGF; 1.  
 KW Merozoite.  
 SQ SEQUENCE 1694 AA; 192766 MW; B51634A49E0F6728 CRC64;

Query Match 57.4%; Score 42.5; DB 5; Length 1694;  
 Best Local Similarity 60.0%; Pred. No. 84;  
 Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 OYKANSKFI-GITE 14  
 ID 09T2T4 PRELIMINARY; PRT; 1704 AA.  
 AC 09T2T4;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE MEROZOITE SURFACE PROTEIN 1 PRECURSOR.  
 GN MSP1.  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5833;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HN2;  
 RA Jiang G., Liu R.Z., Daubenberger C.A., Pluschke G.;  
 RL Submitted (Apr-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF062349; AAC72885.1; -  
 DR InterPro: IPR000561; EGF-like.  
 DR Pfam: PF00008; EGF; 1.  
 KW Merozoite.  
 SQ SEQUENCE 1704 AA; 193762 MW; 3855260DA56FD1D CRC64;

Query Match 57.4%; Score 42.5; DB 5; Length 1704;  
 Best Local Similarity 60.0%; Pred. No. 85;  
 Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 OYKANSKFI-GITE 14  
 ID 09T2T4 PRELIMINARY; PRT; 1704 AA.  
 AC 09T2T4;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE MEROZOITE SURFACE PROTEIN 1 PRECURSOR.  
 GN MSP1.  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5833;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HN2;  
 RA Jiang G., Liu R.Z., Daubenberger C.A., Pluschke G.;  
 RL Submitted (Apr-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF062349; AAC72885.1; -  
 DR InterPro: IPR000561; EGF-like.  
 DR Pfam: PF00008; EGF; 1.  
 KW Merozoite.  
 SQ SEQUENCE 1704 AA; 193762 MW; 3855260DA56FD1D CRC64;

Search completed: January 29, 2002, 11:15:53  
 Job time: 213 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 10:55:58 ; Search time 1760.55 Seconds  
(without alignments)  
2.523 Million cell updates/sec

Title: US-09-763-397A-3

Perfect score: 97  
Sequence: 1 KPLDKFGNIYDYHEH 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_AA\_Main: \*  
1: /cgn2\_6/ptodata/2/paa/PCRNUS\_COMB.pep: \*  
2: /cgn2\_6/ptodata/2/paa/US06\_COMB.pep: \*  
3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep: \*  
4: /cgn2\_6/ptodata/2/paa/US080\_COMB.pep: \*  
5: /cgn2\_6/ptodata/2/paa/US081\_COMB.pep: \*  
6: /cgn2\_6/ptodata/2/paa/US082\_COMB.pep: \*  
7: /cgn2\_6/ptodata/2/paa/US083\_COMB.pep: \*  
8: /cgn2\_6/ptodata/2/paa/US084\_COMB.pep: \*  
9: /cgn2\_6/ptodata/2/paa/US085\_COMB.pep: \*  
10: /cgn2\_6/ptodata/2/paa/US086\_COMB.pep: \*  
11: /cgn2\_6/ptodata/2/paa/US087\_COMB.pep: \*  
12: /cgn2\_6/ptodata/2/paa/US088\_COMB.pep: \*  
13: /cgn2\_6/ptodata/2/paa/US089\_COMB.pep: \*  
14: /cgn2\_6/ptodata/2/paa/US090\_COMB.pep: \*  
15: /cgn2\_6/ptodata/2/paa/US091\_COMB.pep: \*  
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19: /cgn2\_6/ptodata/2/paa/US095\_COMB.pep: \*  
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21: /cgn2\_6/ptodata/2/paa/US097\_COMB.pep: \*  
22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep: \*  
23: /cgn2\_6/ptodata/2/paa/US099\_COMB.pep: \*  
24: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	16	21	US-09-763-397A-3
2	97	100.0	350	21	US-09-763-397A-2
3	54	55.7	277	24	US-60-324-109-22535
4	54	55.7	281	24	US-60-312-544-9219
5	51	52.6	313	15	US-09-134-001C-3628
6	48	49.5	262	15	US-09-198-452A-646
7	48	49.5	262	18	US-09-438-185-608
8	47	48.5	78	17	US-09-328-352-7148
9	46	47.4	102	17	US-09-328-352-5557

	10	46	47.4	134	17	US-09-328-352-5702	Sequence 5702, Ap
	11	46	47.4 <td>141</td> <td>17<td>US-09-328-352-7241</td><td>Sequence 7241, Ap</td></td>	141	17 <td>US-09-328-352-7241</td> <td>Sequence 7241, Ap</td>	US-09-328-352-7241	Sequence 7241, Ap
	12	46	47.4 <td>146</td> <td>17<td>US-09-328-352-4183</td><td>Sequence 4183, Ap</td></td>	146	17 <td>US-09-328-352-4183</td> <td>Sequence 4183, Ap</td>	US-09-328-352-4183	Sequence 4183, Ap
	13	46	47.4 <td>146</td> <td>17<td>US-09-328-352-4906</td><td>Sequence 4906, Ap</td></td>	146	17 <td>US-09-328-352-4906</td> <td>Sequence 4906, Ap</td>	US-09-328-352-4906	Sequence 4906, Ap
	14	46	47.4 <td>191</td> <td>17<td>US-09-328-352-7059</td><td>Sequence 7059, Ap</td></td>	191	17 <td>US-09-328-352-7059</td> <td>Sequence 7059, Ap</td>	US-09-328-352-7059	Sequence 7059, Ap
	15	46	47.4 <td>209</td> <td>17<td>US-09-328-352-7440</td><td>Sequence 7440, Ap</td></td>	209	17 <td>US-09-328-352-7440</td> <td>Sequence 7440, Ap</td>	US-09-328-352-7440	Sequence 7440, Ap
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	17	46	47.4 <td>345</td> <td>17<td>US-09-328-352-5480</td><td>Sequence 5480, Ap</td></td>	345	17 <td>US-09-328-352-5480</td> <td>Sequence 5480, Ap</td>	US-09-328-352-5480	Sequence 5480, Ap
	18	46	47.4 <td>345</td> <td>17<td>US-09-328-352-7604</td><td>Sequence 7604, Ap</td></td>	345	17 <td>US-09-328-352-7604</td> <td>Sequence 7604, Ap</td>	US-09-328-352-7604	Sequence 7604, Ap
	19	45.5	46.9 <td>247</td> <td>17<td>US-09-328-352-7311</td><td>Sequence 7311, Ap</td></td>	247	17 <td>US-09-328-352-7311</td> <td>Sequence 7311, Ap</td>	US-09-328-352-7311	Sequence 7311, Ap
	20	45	46.4 <td>512</td> <td>19<td>US-09-570-581A-938</td><td>Sequence 938, Ap</td></td>	512	19 <td>US-09-570-581A-938</td> <td>Sequence 938, Ap</td>	US-09-570-581A-938	Sequence 938, Ap
	21	44.5	45.9 <td>534</td> <td>1</td> <td>PCT-US01-08631-44074</td> <td>Sequence 44074, A</td>	534	1	PCT-US01-08631-44074	Sequence 44074, A
	22	44	45.4 <td>86</td> <td>22</td> <td>US-60-196-718-6204</td> <td>Sequence 6204, Ap</td>	86	22	US-60-196-718-6204	Sequence 6204, Ap
	23	44	45.4 <td>89</td> <td>22</td> <td>US-09-856-404-20</td> <td>Sequence 5215, Ap</td>	89	22	US-09-856-404-20	Sequence 5215, Ap
	24	44	45.4 <td>138</td> <td>24</td> <td>US-60-215-161-5215</td> <td>Sequence 5215, Ap</td>	138	24	US-60-215-161-5215	Sequence 5215, Ap
	25	44	45.4 <td>309</td> <td>22</td> <td>US-09-856-404-10</td> <td>Sequence 10, Ap</td>	309	22	US-09-856-404-10	Sequence 10, Ap
	26	44	45.4 <td>459</td> <td>19</td> <td>US-09-583-110-4086</td> <td>Sequence 4086, Ap</td>	459	19	US-09-583-110-4086	Sequence 4086, Ap
	27	44	45.4 <td>463</td> <td>15</td> <td>US-09-107-433-4093</td> <td>Sequence 4093, Ap</td>	463	15	US-09-107-433-4093	Sequence 4093, Ap
	28	44	45.4 <td>1263</td> <td>21</td> <td>US-09-733-089-15941</td> <td>Sequence 15941, A</td>	1263	21	US-09-733-089-15941	Sequence 15941, A
	29	44	45.4 <td>1263</td> <td>22</td> <td>US-09-816-660-15941</td> <td>Sequence 15941, A</td>	1263	22	US-09-816-660-15941	Sequence 15941, A
	30	44	45.4 <td>1614</td> <td>21</td> <td>US-09-733-089-200</td> <td>Sequence 200, Ap</td>	1614	21	US-09-733-089-200	Sequence 200, Ap
	31	44	45.4 <td>1614</td> <td>22</td> <td>US-09-816-660-200</td> <td>Sequence 200, Ap</td>	1614	22	US-09-816-660-200	Sequence 200, Ap
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	33	43	44.3 <td>77</td> <td>24</td> <td>US-60-173-469-1167</td> <td>Sequence 1167, Ap</td>	77	24	US-60-173-469-1167	Sequence 1167, Ap
	34	43	44.3 <td>77</td> <td>24</td> <td>US-60-188-162-3835</td> <td>Sequence 3835, Ap</td>	77	24	US-60-188-162-3835	Sequence 3835, Ap
	35	43	44.3 <td>78</td> <td>24</td> <td>US-60-169-840-4940</td> <td>Sequence 4940, Ap</td>	78	24	US-60-169-840-4940	Sequence 4940, Ap
	36	43	44.3 <td>199</td> <td>15</td> <td>US-09-107-532-5931</td> <td>Sequence 5931, Ap</td>	199	15	US-09-107-532-5931	Sequence 5931, Ap
	37	43	44.3 <td>199</td> <td>15</td> <td>US-09-107-532A-5931</td> <td>Sequence 5931, Ap</td>	199	15	US-09-107-532A-5931	Sequence 5931, Ap
	38	43	44.3 <td>243</td> <td>24</td> <td>US-60-241-098-14</td> <td>Sequence 14, Ap</td>	243	24	US-60-241-098-14	Sequence 14, Ap
	39	43	44.3 <td>329</td> <td>1</td> <td>PCT-US01-03404B-14</td> <td>Sequence 14, Ap</td>	329	1	PCT-US01-03404B-14	Sequence 14, Ap
	40	43	44.3 <td>3952</td> <td>24</td> <td>US-60-173-464-9205</td> <td>Sequence 9205, Ap</td>	3952	24	US-60-173-464-9205	Sequence 9205, Ap
	41	43	44.3 <td>4010</td> <td>24</td> <td>US-60-191-637-11384</td> <td>Sequence 11384, A</td>	4010	24	US-60-191-637-11384	Sequence 11384, A
	42	43	44.3 <td>4010</td> <td>24</td> <td>US-60-191-681-8915</td> <td>Sequence 8915, Ap</td>	4010	24	US-60-191-681-8915	Sequence 8915, Ap
	43	42	43.3 <td>123</td> <td>1</td> <td>PCT-US97-02318-350</td> <td>Sequence 350, Ap</td>	123	1	PCT-US97-02318-350	Sequence 350, Ap
	44	42	43.3 <td>123</td> <td>13</td> <td>US-08-903-470-350</td> <td>Sequence 350, Ap</td>	123	13	US-08-903-470-350	Sequence 350, Ap
	45	42	43.3 <td>181</td> <td>1</td> <td>PCT-US00-06112-1033</td> <td>Sequence 1033, Ap</td>	181	1	PCT-US00-06112-1033	Sequence 1033, Ap

#### ALIGNMENTS

RESULT 1  
US-09-763-397A-3  
Sequence 3, Application US/09763397A  
GENERAL INFORMATION:  
APPLICANT: The Government of the United States of America, as represented by the  
APPLICANT: Secretary of the Department of Health and Human Services, Centers for  
APPLICANT: Control and Prevention  
APPLICANT: Lal, Altaf A.  
APPLICANT: Ping Shi, Ya  
APPLICANT: Hashain, Seyed E.  
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa  
FILE REFERENCE: 6395-57049  
CURRENT APPLICATION NUMBER: US/09/763, 397A  
CURRENT FILING DATE: 2001-02-16  
PRIOR APPLICATION NUMBER: US 60/097, 703  
PRIOR FILING DATE: 1998-08-21  
PRIOR APPLICATION NUMBER: PCT / US99/18869  
PRIOR FILING DATE: 1999-08-19  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Plasmodium falciparum  
US-09-763-397A-3

Query Match 100.0%: Score 97; DB 21; Length 16;  
Best Local Similarity 100.0%: Pred. No. 1.7e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 KPLDKFGNIYDYHEH 16

```

Db      1 KPLDKFGNIYDYHYEH 16

```

RESULT 2  
HE-09-763

US-09-763-397A-2  
; Sequence 2, Application US/09763397A  
GENERAL INFORMATION:

```

GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
APPLICANT: Control and Prevention
APPLICANT: Ial, Altaf A.
APPLICANT: Ping Shi, Ya
APPLICANT: Hasnain, Seyed E.
FILE REFERENCE: 6395-57049
CURRENT APPLICATION NUMBER: US/09/763.397A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 350
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant DNA/Protein
US-09-763-397A-2

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Query Match	100.0%;	Score 97;	DB 21;	Length 350;
Best Local Similarity	100.0%;	Pred. No. 5.4e-07;		
Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY      1 KPLDKFGNIYDYHYEH 16
          |||
Db     283 KPLDKFGNIYDYHYEH 298
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### RESULT 3

```

US-60-324-109-22535
Sequence 22535, Application US/60324109
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(53726)B
CURRENT APPLICATION NUMBER: US/60/324,109
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ. ID NOS: 33196
SEQ. ID NO 22535
LENGTH: 277
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
US-60-324-109-22535

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Query Match	55.7%;	Score 54;	DB 24;	Length 277;
Best Local Similarity	53.3%;	Pred. NO. 3.7;		
Matches	8;	Conservative	3;	Mismatches 4;
				Indels 0;
				Gaps 0

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QY      1 KPLDKFGNIYDYHYE 15
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Db      50 RPYGVNFKNSYDYHYQ 64
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#### RESULT 4

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US-60-312-544-9219
Sequence 9219, Application US/60312544
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovacic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(527226)A
CURRENT APPLICATION NUMBER: US/60/312,544
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 10730
SEQ ID NO 9219
LENGTH: 281
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: LIB3170-048-D4_FLI
US-60-312-544-9219

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Query Match	55.7%;	Score 54;	DB 24;	Length 281;
Best Local Similarity	53.3%;	Pred. NO. 3.8;		
Matches	8;	Conservative	3;	Mismatches 4;
				Indels 0;
				Gaps 0;

```
QY      1 KPLDKFGNIYDYHYE 15
          ::| | | | | | |
Db     50 RPYGNEFKNSYDYHYQ 64
```

RESULT 5  
US-09-134-

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? Sequence 3628, Application US/09134/001C
? GENERAL INFORMATION:
? APPLICANT: Lynn Doucette-Stamm et al
? TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
? TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
? FILE REFERENCE: GTC-007
? CURRENT APPLICATION NUMBER: US/09/134,001C
? CURRENT FILING DATE: 1998-08-13
? PRIOR APPLICATION NUMBER: US 60/064,964
? PRIOR FILING DATE: 1997-11-08
? PRIOR APPLICATION NUMBER: US 60/055,779
? PRIOR FILING DATE: 1997-08-14
? NUMBER OF SEQ ID NOS: 5674
? SEQ ID NO 3628
? LENGTH: 313
? TYPE: PRF
? ORGANISM: Staphylococcus epidermidis
? US-09-134-001C-3628

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Query Match	52.6%;	Score 51;	DB 15;	Length 313;
Best Local Similarity	60.0%;	Pred. No. 13;		
Matches	9;	Conservative	3;	Mismatches 3;
			Indels	0;
			Gaps	0

```
QY      1 KPLDKFGNIYDYHYE 15
          :|:|:|:|:|:|:|
Db      42 QPVDKFGEIYDLNPE 56
```

## RESULT 6

```

US-09-198-452A-646
; Sequence 646, Application US/09198452A
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection

```

FILE REFERENCE: 9710-003-999  
CURRENT APPLICATION NUMBER: US/09/198-452A  
CURRENT FILING DATE: 1998-11-24  
NUMBER OF SEQ ID NOS: 6849  
SEQ ID NO 646  
LENGTH: 262  
TYPE: PRT  
ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-646

Query Match 49.5%; Score 48; DB 15; Length 262;  
Best Local Similarity 57.1%; Pred. No. 32;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 KPLDKFGNIYDYH 14  
DB 233 RPIDGFGNIRGIHY 246

RESULT 7  
US-09-438-185-608  
Sequence 608, Application US/09438185  
GENERAL INFORMATION:  
APPLICANT: Stephens, Richard  
APPLICANT: Mitchell, Wayne  
APPLICANT: Kalman, Sue  
APPLICANT: Davis, Ronald  
TITLE OF INVENTION: The Regents of the University of California  
FILE REFERENCE: 018941-000411US  
CURRENT APPLICATION NUMBER: US/09/438,185  
CURRENT FILING DATE: 1999-11-11  
PRIOR APPLICATION NUMBER: US 60/108,279  
PRIOR FILING DATE: 1998-11-12  
PRIOR APPLICATION NUMBER: US 60/128,606  
PRIOR FILING DATE: 1999-04-08  
NUMBER OF SEQ ID NOS: 1074  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 608  
LENGTH: 262  
TYPE: PRT  
ORGANISM: Chlamydia pneumoniae  
US-09-438-185-608

Query Match 49.5%; Score 48; DB 18; Length 262;  
Best Local Similarity 57.1%; Pred. No. 32;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 KPLDKFGNIYDYH 14  
DB 233 RPIDGFGNIRGIHY 246

RESULT 8  
US-09-328-352-7148  
Sequence 7148, Application US/09328352  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 7148  
LENGTH: 78  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-7148

Query Match 48.5%; Score 47; DB 17; Length 78;  
Best Local Similarity 56.2%; Pred. No. 12;  
Matches 9; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

OY 2 PLDKFGNIYDYH--YE 15  
DB 57 PLEKFAQLVDYHMAVE 72

RESULT 9  
US-09-328-352-5557  
Sequence 5557, Application US/09328352  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 5557  
LENGTH: 102  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-5557

Query Match 47.4%; Score 46; DB 17; Length 102;  
Best Local Similarity 58.3%; Pred. No. 23;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 PLDKFGNIYDYH 13  
DB 81 PLEKFAQLVDYH 92

RESULT 10  
US-09-328-352-5702  
Sequence 5702, Application US/09328352  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 5702  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-5702

Query Match 47.4%; Score 46; DB 17; Length 134;  
Best Local Similarity 58.3%; Pred. No. 32;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 PLDKFGNIYDYH 13  
DB 113 PLEKFAQLVDYH 124

RESULT 11  
US-09-328-352-7241  
Sequence 7241, Application US/09328352  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 7241  
LENGTH: 141  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-7241

Query Match 47.4%; Score 46; DB 17; Length 141;  
Best Local Similarity 58.3%; Pred. No. 34;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 PLDKFGNIYDYH 13  
||:| : |||  
Db 120 PLEKFAQLVDYH 131

RESULT 12  
US-09-328-352-4183  
; Sequence 4183, Application US/09328352  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 4183  
; LENGTH: 146  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-4183

Query Match 47.4%; Score 46; DB 17; Length 146;  
Best Local Similarity 58.3%; Pred. No. 35;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 PLDKFGNIYDYH 13  
||:| : |||  
Db 125 PLEKFAQLVDYH 136

RESULT 13  
US-09-328-352-4906  
; Sequence 4906, Application US/09328352  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 4906  
; LENGTH: 146  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-4906

Query Match 47.4%; Score 46; DB 17; Length 146;  
Best Local Similarity 58.3%; Pred. No. 35;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 PLDKFGNIYDYH 13  
||:| : |||  
Db 125 PLEKFAQLVDYH 136

RESULT 14  
US-09-328-352-7059

; Sequence 7059, Application US/09328352  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 7059  
; LENGTH: 191  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-7059

Query Match 47.4%; Score 46; DB 17; Length 191;  
Best Local Similarity 58.3%; Pred. No. 48;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 PLDKFGNIYDYH 13  
||:| : |||  
Db 170 PLEKFAQLVDYH 181

RESULT 15  
US-09-328-352-7440  
; Sequence 7440, Application US/09328352  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 7440  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-7440

Query Match 47.4%; Score 46; DB 17; Length 209;  
Best Local Similarity 58.3%; Pred. No. 53;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 PLDKFGNIYDYH 13  
||:| : |||  
Db 188 PLEKFAQLVDYH 199

Search completed: January 29, 2002, 10:55:59  
Job time: 2395 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 10:58:07 ; Search time 120.95 Seconds  
(without alignments)  
4.841 Million cell updates/sec

Title: US-09-763-397A-3  
Perfect score: 97  
Sequence: 1 KPLDKRGNITYDYHEH 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 173191 seqs, 36597120 residues

Total number of hits satisfying chosen parameters: 173191

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_AA-New:\*  
1: /cgn2\_6/ptodata/2/paa/PCY\_NEW\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep:\*  
7: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	45.4	138	5	US-09-897-516-5215
2	44	45.4	459	5	US-09-815-242-13229
3	44	45.4	1404	5	US-09-708-427-21300
4	44	45.4	1420	5	US-09-708-427-11605
5	44	45.4	1517	5	US-09-708-427-11604
6	44	45.4	1519	5	US-09-708-427-11603
7	41	42.3	41	5	US-09-620-111B-8023
8	41	42.3	249	5	US-09-708-427-82968
9	41	42.3	359	5	US-09-708-427-65147
10	41	42.3	369	5	US-09-708-427-65146
11	41	42.3	395	5	US-09-708-427-65145
12	41	42.3	442	5	US-09-708-427-2795
13	41	42.3	497	5	US-09-708-427-2794
14	41	42.3	521	5	US-09-708-427-2793
15	40	41.2	212	5	US-09-708-427-68197
16	40	41.2	364	5	US-09-708-427-68198
17	39	40.2	121	6	US-10-015-127-11238
18	39	40.2	261	5	US-09-708-427-72557
19	39	40.2	262	5	US-09-708-427-67046
20	39	40.2	262	5	US-09-708-427-83736
21	39	40.2	279	5	US-09-708-427-67045
22	39	40.2	279	5	US-09-708-427-83735
23	39	40.2	303	5	US-09-708-427-67044
24	39	40.2	303	5	US-09-708-427-83734
25	39	40.2	393	5	US-09-708-427-17303
26	39	40.2	426	5	US-09-708-427-1466

27	39	40.2	447	5	US-09-708-427-17302	Sequence 17302, A
28	39	40.2	468	5	US-09-708-427-1465	Sequence 1465, Ap
29	39	40.2	481	5	US-09-708-427-17301	Sequence 17301, A
30	39	40.2	488	5	US-09-708-427-1464	Sequence 1464, Ap
31	39	40.2	1010	6	US-10-015-127-9620	Sequence 9820, Ap
32	39	40.2	1563	5	US-09-708-427-3644	Sequence 3644, Ap
33	39	40.2	1591	5	US-09-708-427-3643	Sequence 3643, Ap
34	39	40.2	1609	5	US-09-708-427-3642	Sequence 3642, Ap
35	38.5	39.7	172	5	US-09-985-153-91	Sequence 91, Appl
36	38.5	39.7	172	5	US-09-985-153-135	Sequence 135, Appl
37	38.5	39.7	267	5	US-09-985-153-70	Sequence 70, Appl
38	38	39.2	180	5	US-09-708-427-69129	Sequence 69129, A
39	38	39.2	187	5	US-09-708-427-80349	Sequence 80349, A
40	38	39.2	197	5	US-09-708-427-20520	Sequence 20520, A
41	38	39.2	207	5	US-09-708-427-20518	Sequence 20518, A
42	38	39.2	211	5	US-09-708-427-69128	Sequence 69128, A
43	38	39.2	218	5	US-09-708-427-80348	Sequence 80348, A
44	38	39.2	240	5	US-09-708-427-24797	Sequence 24797, A
45	38	39.2	255	5	US-09-708-427-24796	Sequence 24796, A

#### ALIGNMENTS

```
RESULT 1
US-09-897-516-5215
; Sequence 5215, Application US/09897516
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Hinkle, Joseph E.
; APPLICANT: Krasomil-Osterfeld, Karina C.
; APPLICANT: Malvar, Thomas M.
; APPLICANT: Slater, Steven C.
; APPLICANT: Spiridonov, Sergei
; TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
; FILE REFERENCE: 38-21(51847)B
; CURRENT APPLICATION NUMBER: US/09/897,516
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215, 161
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 8409
; SEQ ID NO 5215
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Xenorhabdus sp.
US-09-897-516-5215

Query Match 45.4%; Score 44; DB 5; Length 138;
Best Local Similarity 70.0%; Pred. No. 4.9;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 GNIYDYHEH 16
DB 28 GKAYDYHREH 37

RESULT 2
US-09-815-242-13229
; Sequence 13229, Application US/09815242
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes In
; PROKARYOTES
```

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; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13229
; LENGTH: 459
; TYPE: PRF
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13229
```

```
Query Match          45.4%; Score 44; DB 5; Length 459;
Best Local Similarity 58.3%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
OY 5 KEGNIYDYHEH 16
    11 11111
Db 172 EFGFYDHYHYPH 183
```

```
RESULT 3
US-09-708-427-21300
; Sequence 21300, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 85364
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21300
; LENGTH: 1404
; TYPE: PRF
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..1404
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: 1..1404
; OTHER INFORMATION: Ceres Seq. ID 1839339
US-09-708-427-21300
```

```
Query Match          45.4%; Score 44; DB 5; Length 1404;
Best Local Similarity 46.7%; Pred. No. 66;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
```

```
OY 1 KPLDKFGNIYDYHVE 15
    11 1: :111:1
Db 102 KPSKKYKKLYDYFFE 116
```

```
RESULT 4
US-09-708-427-11605
; Sequence 11605, Application US/09708427
```

```
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 85364
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11605
; LENGTH: 1420
; TYPE: PRF
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..1420
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: 1..1420
; OTHER INFORMATION: Ceres Seq. ID 1823474
US-09-708-427-11605
```

```
Query Match          45.4%; Score 44; DB 5; Length 1420;
Best Local Similarity 46.7%; Pred. No. 67;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
```

```
OY 1 KPLDKFGNIYDYHVE 15
    11 1: :111:1
Db 62 KPSKKYKKLYDYFFE 76
```

```
RESULT 5
US-09-708-427-11604
; Sequence 11604, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 85364
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11604
; LENGTH: 1517
; TYPE: PRF
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..1517
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: 1..1517
; OTHER INFORMATION: Ceres Seq. ID 1823473
US-09-708-427-11604
```

```
Query Match          45.4%; Score 44; DB 5; Length 1517;
Best Local Similarity 46.7%; Pred. No. 72;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
```

```
OY 1 KPLDKFGNIYDYHVE 15
    11 1: :111:1
Db 159 KPSKKYKKLYDYFFE 173
```

```
RESULT 6
US-09-708-427-11603
; Sequence 11603, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
```

```
; TITLE OF INVENTION: THEREBY
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 85364
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11603
; LENGTH: 1519
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..1519
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: 1..1519
; OTHER INFORMATION: Ceres Seq. ID 1823472
; US-09-708-427-11603
```

```
Query Match          45.4%; Score 44; DB 5; Length 1519;
Best Local Similarity 46.7%; Pred. No. 72;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
```

```
OY 1 KPLDKFGNIYDYH 15
    |||::|||:|
DB 161 KPSKKYKKKYDYFFE 175
```

```
RESULT 7
; US-09-620-111B-8023
; Sequence 8023, Application US/09620111B
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1070P
; CURRENT APPLICATION NUMBER: US/09/620,111B
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 9298
; SEQ ID NO 8023
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..41
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: 1..41
; OTHER INFORMATION: Ceres Seq. ID 1342121
; US-09-620-111B-8023
```

```
Query Match          42.3%; Score 41; DB 5; Length 41;
Best Local Similarity 46.2%; Pred. No. 3.8;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 KPLDKFGNIYDYH 13
    |||::|||:|
DB 7 RPLDHPADLYDFH 19
```

```
RESULT 8
; US-09-708-427-82968
; Sequence 82968, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000-11-09
```

```
; NUMBER OF SEQ ID NOS: 85364
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82968
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..249
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: 1..249
; OTHER INFORMATION: Ceres Seq. ID 1961854
; US-09-708-427-82968
```

```
Query Match          42.3%; Score 41; DB 5; Length 249;
Best Local Similarity 46.2%; Pred. No. 29;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 KPLDKFGNIYDYH 13
    |||::|||:|
DB 7 RPLDHPADLYDFH 19
```

```
RESULT 9
; US-09-708-427-65147
; Sequence 65147, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 85364
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65147
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..359
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: 1..359
; OTHER INFORMATION: Ceres Seq. ID 1928281
; US-09-708-427-65147
```

```
Query Match          42.3%; Score 41; DB 5; Length 359;
Best Local Similarity 58.3%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 4 DKFGNIYDYH 15
    |||::|||:|
DB 77 DEYGYGYDYDE 88
```

```
RESULT 10
; US-09-708-427-65146
; Sequence 65146, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 85364
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65146
```

```
LENGTH: 369
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..369
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..369
OTHER INFORMATION: Ceres Seq. ID 1928280
US-09-708-427-65146
```

```
Query Match          42.3% Score 41; DB 5; Length 369;
Best Local Similarity 58.3% Pred. No. 44;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 4 DKFGNIYDYHYE 15
    ||| ||| |||
Db 87 DEYGYDYDYDE 98
```

```
RESULT 11
US-09-708-427-65145
Sequence 65145, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 65145
LENGTH: 395
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..395
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..395
OTHER INFORMATION: Ceres Seq. ID 1928279
US-09-708-427-65145
```

```
Query Match          42.3% Score 41; DB 5; Length 395;
Best Local Similarity 58.3% Pred. No. 48;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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```
OY 4 DKFGNIYDYHYE 15
    ||| ||| |||
Db 113 DEYGYDYDYDE 124
```

```
RESULT 12
US-09-708-427-2795
Sequence 2795, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2795
LENGTH: 442
TYPE: PRT
ORGANISM: Arabidopsis thaliana
```

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FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..442
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..442
OTHER INFORMATION: Ceres Seq. ID 1809716
US-09-708-427-2795
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Query Match          42.3% Score 41; DB 5; Length 442;
Best Local Similarity 53.8% Pred. No. 54;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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```
OY 1 KPLDKFGNIYDYH 13
    ||| : |||
Db 186 KPLDHPADYFDYH 198
```

```
RESULT 13
US-09-708-427-2794
Sequence 2794, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2794
LENGTH: 497
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..497
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..497
OTHER INFORMATION: Ceres Seq. ID 1809715
US-09-708-427-2794
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```
Query Match          42.3% Score 41; DB 5; Length 497;
Best Local Similarity 53.8% Pred. No. 62;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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```
OY 1 KPLDKFGNIYDYH 13
    ||| : |||
Db 241 KPLDHPADYFDYH 253
```

```
RESULT 14
US-09-708-427-2793
Sequence 2793, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2793
LENGTH: 521
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..521
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```

; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..521
; OTHER INFORMATION: Ceres Seq. ID 1809714
US-09-708-427-2793

```

```

Query Match          42.3%; Score 41; DB 5; Length 521;
Best Local Similarity 53.8%; Pred. No. 65;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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```

OY 1 KPLDKFGNIYDYH 13
    |||| : |||
Db 265 KPLDHPADYFDYH 277

```

```

RESULT 15
US-09-708-427-68198
; Sequence 68198, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ. ID NOS: 85364
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68198
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..212
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..212
; OTHER INFORMATION: Ceres Seq. ID 1934091
US-09-708-427-68198

```

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Query Match          41.2%; Score 40; DB 5; Length 212;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 4 DKFGNIV 10
    |||||
Db 44 DKFGNIV 50

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Search completed: January 29, 2002, 10:58:07  
 Job time: 2503 sec

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FT      Region      104
FT      /label= artifact
FT      /note= "see comments"
FT      Region      105..209
FT      /label= AAs 19-123 of CS protein
FT      /note= "Region I contg. flanking region less
FT      signal sequence"
FT      Region      210
FT      /label= artifact
FT      /note= "see comments"
FT      Region      211..335
FT      /label= AAs 288-412 of CS protein
FT      /note= "Region II flanking region"
FT      EP432965-A.
FT      19-JUN-1991.
FT      06-DEC-1990; 90EP-0313257.
FT      08-DEC-1989; 89US-0447746.
FT      (SMIK ) SMITHKLINE BEECHAM.
FT      (USSA ) US SEC OF THE ARMY.
FT      (BIOM-) BIOMEDICAL RES INST.
FT      Gross MS, Gordon DM, Hollingdale MR;
FT      WPI; 1991-179771/25.
FT      Polypeptide comprising immunogenic determinants from P falciparum
FT      - for vaccine against malaria infection in humans.
FT      Example 4; Page 11; 18pp; English.
FT      The polypeptide is prep. by genetic engineering of genes encoding
FT      the P. falciparum circumsporozoite (CS) protein [Dane et al.,
FT      Science 225 : 593 (1984)], and the influenza virus non-structural
FT      protein 1 (NSI), [Baez et al., Nucleic Acids Research, 8 : 5845
FT      (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NSI
FT      (NSI-81) is linked to a synthetic sequence encoding four repeat
FT      units from the immunodominant region, which in turn is linked via
FT      a synthetic sequence to DNA encoding region I contg. flanking
FT      region less the 18 AA signal region. This is linked to DNA
FT      encoding Region II-contg. flanking region. The pro residue sep-
FT      arating the Asp (at the C-terminal of the linker) from the Region
FT      I-contg. CS flanking region is an artifact of a filled-in BamHI
FT      site; the Gly separating the Region I and II-contg. CS flanking
FT      regions is an artifact of a synthetic FokI/ThiIII I linker. The
FT      peptide can be used in a vaccine for protection against malaria.
FT      See also AAR12306-R12311 and AAR13175-R13179.
FT      Sequence 335 AA:
FT      Query Match 100.0%; Score 127; DB 12; Length 335;
FT      Best Local Similarity 100.0%; Pred. No. 1,7e-10;
FT      Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT      Oy 1 kPKDELVDYNDIEKKIKCMKES 23
FT      Db 291 kPKDELVDYNDIEKKIKCMKES 313
FT      RESULT 8
FT      AAR13179
FT      ID AAR13179 standard; Protein; 335 AA.
FT      AC AAR13179;
FT      XX 29-AUG-1991 (first entry)
FT      DT NS1_81(NWDP)4RLfAuth.
FT      DE

```

```

XX      XX      Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;
XX      KW      hybrid; Influenza virus; non-structural protein 1; fusion.
XX      OS      Plasmodium falciparum.
XX      OS      Influenza virus (A/PR/8/34).
XX      Key      Location/Qualifiers
XX      Region      1..81
XX      /label= N-terminal of NSI
XX      /note= "Influenza virus nonstructural protein 1"
XX      Region      82..97
XX      /label= immunodominant repeat region
XX      /note= "four variant tetrapeptide repeat units"
XX      Peptide      98..103
XX      /label= synthetic linker
XX      Region      104
XX      /label= artifact
XX      /note= "see comments"
XX      Region      105..209
XX      /label= AAs 19-123 of CS protein
XX      /note= "Region I contg. flanking region less
XX      signal sequence"
XX      Region      210
XX      /label= artifact
XX      /note= "see comments"
XX      Region      211..335
XX      /label= AAs 288-412 of CS protein
XX      /note= "Region II flanking region"
XX      EP432965-A.
XX      19-JUN-1991.
XX      06-DEC-1990; 90EP-0313257.
XX      08-DEC-1989; 89US-0447746.
XX      (SMIK ) SMITHKLINE BEECHAM.
XX      (USSA ) US SEC OF THE ARMY.
XX      (BIOM-) BIOMEDICAL RES INST.
XX      Gross MS, Gordon DM, Hollingdale MR;
XX      WPI; 1991-179771/25.
XX      Polypeptide comprising immunogenic determinants from P falciparum
XX      - for vaccine against malaria infection in humans.
XX      Example 5; Page 11; 18pp; English.
XX      The polypeptide is prep. by genetic engineering of genes encoding
XX      the P. falciparum circumsporozoite (CS) protein [Dane et al.,
XX      Science 225 : 593 (1984)], and the influenza virus non-structural
XX      protein 1 (NSI), [Baez et al., Nucleic Acids Research, 8 : 5845
XX      (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NSI
XX      (NSI-81) is linked to a synthetic sequence encoding four repeat
XX      units (the variant form) from the immunodominant region, which in
XX      turn is linked via a synthetic sequence to DNA encoding Region I
XX      contg. flanking region less the 18 AA signal region. This is
XX      linked to DNA encoding Region II-contg. flanking region. The pro
XX      residue separating the Asp (at the C-terminal of the linker) from
XX      the Region I-contg. CS flanking region is an artifact of a filled-
XX      in BamHI site; the Gly separating the Region I and II-contg. CS
XX      flanking regions is an artifact of a synthetic FokI/ThiIII I
XX      linker. The peptide can be used in a vaccine for protection
XX      against malaria.
XX      See also AAR12306-R12311 and AAR13175-R13178.
XX      Sequence 335 AA:
XX      Query Match 100.0%; Score 127; DB 12; Length 335;

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Best Local Similarity 100.0%; Pred. No. 1.7e-10;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPRDELVDYNDIEKKICKMEKCS 23  
DB 291 KPKDELVDYNDIEKKICKMEKCS 313

## RESULT 9

AA70278  
ID AAY70278 standard; protein: 350 AA.

XX AAY70278;

DT 06-JUN-2000 (first entry)

XX Recombinant vaccine CDC/NITMAYVAC-1.

KM Recombinant protein: CDC/NITMAYVAC-1; multivalent; malarial; vaccine;

KM T-cell epitope; tetanus toxoid; antigenic epitope; treatment; vaccine;

KM Circumsporozoite protein: CSP; sporozoite surface protein-2; SSP-2;

KM Liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1;

KM Apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175;

KM EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen;

KM PIG27; antiparasitic; prevention; anti-CDC/NITMAYVAC-1 antibody;

KM honey bee.

XX Chimeric - Apis sp.

OS Chimeric - Clostridium tetani.

XX Chimeric - Plasmodium falciparum.

XX Key location/Qualifiers

FT Peptide 1..22 Melittin-signal-peptide

FT Protein /note="Derived from Honey Bee"

FT /label="Mature\_CDC/NITMAYVAC-1"

FT /note="Recombinant multivalent malarial vaccine"

XX WO200011179-A1.

XX 02-MAR-2000.

XX 19-AUG-1999; 99WO-US18869.

XX 21-AUG-1998; 98US-0097703.

XX (NAIN-) NAT INST IMMUNOLOGY.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Tal AA, Shi YP, Hasnain SE;

XX WPI: 2000-237654/20.

XX N-PSDB; AAZ51336.

XX Novel recombinant protein as vaccine for treating malarial infection

XX comprises antigenic peptides obtained from different stages of

XX plasmodium falciparum life cycle. -

XX Claim 3; Page 43-44; 52pp; English.

XX The present sequence is that of recombinant protein CDC/NITMAYVAC-1,

XX which is a multivalent, multistage malarial vaccine. The recombinant

XX protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope

XX from tetanus toxoid and 21 antigenic epitopes from circumsporozoite

XX protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage

XX antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical

XX membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175),

XX rhoptry associated protein-1 (RAP-1) and gamete specific antigen, PIG27.

XX These epitopes were obtained at different stages of the life cycle of

XX plasmodium falciparum. CDC/NITMAYVAC-1 vaccine has antiparasitic

XX activity and can be used for treatment and prevention of malarial

XX infections. Anti-CDC/NITMAYVAC-1 antibodies can be used for detecting

CC P. falciparum in biological samples.

XX Sequence 350 AA;

QY Query Match 100.0%; Score 127; DB 21; Length 350;

Best Local Similarity 100.0%; Pred. No. 1.8e-10;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 51 KPRDELVDYNDIEKKICKMEKCS 73

## RESULT 10

AA83144  
ID AAP83144 standard; protein: 411 AA.

XX AAP83144;

DT 20-NOV-1990 (first entry)

XX Sequence encoded by the circumsporozoite (CS) gene from

XX Plasmodium falciparum.

XX Vaccine; antigen; immunogen; probe; hybridisation;

XX immunosassay; diagnosis.

XX Plasmodium falciparum.

XX Key location/Qualifiers

FT Region 106..120

FT /note="Region 1"

FT Region 147..206

FT /note="Repeat region, repeat unit = NAMP"

FT Region 123..146

FT /note="Repeat region, repeat unit = NAMPNDP"

FT Region 211..286

FT /note="Repeat region, repeat unit = NAMP"

XX EP278940-A.

XX 17-AUG-1988.

XX 25-JAN-1988; 88EP-0870008.

XX 30-JAN-1987; 87US-0009325.

XX (SMRK ) SMITH KLINE-RIT.

XX Cabazon T, De Wilde M, Harford N;

XX WPI: 1988-229751/33.

XX N-PSDB; AAN81108.

XX DNA encoding hepatitis B virus antigens and hybrids contg. them -

XX used for expression in yeast to obtain vaccines and bivalent

XX vaccines

XX Example; Fig 3Aa-3Af; 101pp; English.

XX Sequence of the CS gene (AAN81108) is from lambda-mp1. A recombinant

XX DNA molecule is claimed, comprising functional DNA coding sequence fused,

XX in phase, to a portion of the Pre-S2 region of a hepatitis B virus (HBV)

XX Pre-S2 protein coding sequence. The functional DNA coding sequence

XX comprises the Pre-S2 coding sequence, the CS protein coding sequence or

XX Pre-S1-Pre-S2 coding sequence, the CS protein coding sequence or

XX an HIV envelope gene sequence, e.g. HIV C7 protein coding region, HIV

XX Peptide 121 coding region, or HIV Dreesman peptide coding region.

XX Sequence 411 AA;



RA Olafsson P., Matile H., Certa U.;  
RT "Plasmodium falciparum: the repetitive MSA-1 surface protein of the  
RT RO-71 isolate is recognized by mouse antibody against the  
RT nonrepetitive repeat block of RO-33."  
RL Exp. Parasitol. 74:381-389(1992).  
DR EMBL: X61930; CAA43932.1; -  
DR InterPro: IPR000087; Collagen.  
FT NON\_TER 1087 1087  
SQ SEQUENCE 1087 AA; 123911 MW; 5518852133C01B33 CRC64;

Query Match 57.4%; Score 42.5; DB 5; Length 1087;  
Best Local Similarity 60.0%; Pred. No. 53;  
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

OY 1 QYIKANSKFI-GITE 14  
DB 1009 QFVKSNSKVITGLTE 1023

RESULT 13  
O9T2T5 PRELIMINARY; PRT; 1694 AA.  
AC O9T2T5;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE MEROZOITE SURFACE PROTEIN 1 PRECURSOR.  
GN MSP1.  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HN1;  
RA Jiang G., Liu R.Z., Daubenberger C.A., Pluschke G.;  
RL Submitted (APR-1998) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF062348; AAC72884.1; -  
DR InterPro: IPR000561; EGF-like.  
DR Pfam: PF00008; EGF; 1.  
KW Merozoite.  
SQ SEQUENCE 1694 AA; 192794 MW; 84CF0E709F5673B CRC64;

Query Match 57.4%; Score 42.5; DB 5; Length 1694;  
Best Local Similarity 60.0%; Pred. No. 84;  
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

OY 1 QYIKANSKFI-GITE 14  
DB 995 QFVKSNSKVITGLTE 1009

RESULT 14  
O9NHX1 PRELIMINARY; PRT; 1694 AA.  
AC O9NHX1;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE MAJOR MEROZOITE SURFACE ANTIGEN.  
GN GPI95.  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FCCL/HN;  
RA Shan Z.X., Yu X.B., Li X.R., Ma C.L., Fang J.M.;  
RT "Molecular cloning and sequence analysis of major merozoite surface  
RT antigen(gpi95)gene of Plasmodium falciparum isolate FCC1/HN."  
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF218248; AAF27526.1; -

DR InterPro: IPR000561; EGF-like.  
DR Pfam: PF00008; EGF; 1.  
KW Merozoite.  
SQ SEQUENCE 1694 AA; 192766 MW; B51634A49E0F6728 CRC64;

Query Match 57.4%; Score 42.5; DB 5; Length 1694;  
Best Local Similarity 60.0%; Pred. No. 84;  
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

OY 1 QYIKANSKFI-GITE 14  
DB 995 QFVKSNSKVITGLTE 1009

RESULT 15  
O9T2T4 PRELIMINARY; PRT; 1704 AA.  
AC O9T2T4;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE MEROZOITE SURFACE PROTEIN 1 PRECURSOR.  
GN MSP1.  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HN2;  
RA Jiang G., Liu R.Z., Daubenberger C.A., Pluschke G.;  
RL Submitted (APR-1998) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF062349; AAC72885.1; -  
DR InterPro: IPR000561; EGF-like.  
DR Pfam: PF00008; EGF; 1.  
KW Merozoite.  
SQ SEQUENCE 1704 AA; 193762 MW; 38526DDDA56FD1D CRC64;

Query Match 57.4%; Score 42.5; DB 5; Length 1704;  
Best Local Similarity 60.0%; Pred. No. 85;  
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

OY 1 QYIKANSKFI-GITE 14  
DB 1005 QFVKSNSKVITGLTE 1019

Search completed: January 29, 2002, 11:15:53  
Job time: 213 sec



ID 09XRJ9 PRELIMINARY: PRT: 71 AA.  
 AC 09XRJ9  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE MHC CLASS II BETA 1 (FRAGMENT).  
 GN SANA.  
 OS Salvelinus namaycush (lake trout).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.  
 NCBI\_TaxID=8040.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Dorschner M.O., Duris T., Phillips R.B.;  
 RT "Diversity of a lake trout Mhc class II gene."  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- MISCELLANEOUS: FOUND N-TERMINAL TO IMMUNOGLOBULIN AND MAJOR  
 CC HISTOCOMPATIBILITY COMPLEX DOMAIN (BY SIMILARITY).  
 CC -1- SIMILARITY: TO CLASS II HISTOCOMPATIBILITY ANTIGEN, BETA CHAIN.  
 CC BETA-1 DOMAIN INTERPRO FAMILY.  
 DR EMBL: AF130026; AAD20889.1;  
 DR InterPro: IPR000353; MHC\_II\_beta.  
 DR Pfam: PF00969; MHC\_II\_beta.1.  
 DR ProDom: PD000328; MHC\_II\_beta.1.  
 DR Glycoprotein: MHC II; Transmembrane.  
 FT NON\_TER 1 71  
 FT SEQUENCE 71 AA: 8002 MW: E3095286582A9F2D CRC64;

Query Match 60.1%; Score 44.5; DB 7; Length 71;  
 Best Local Similarity 55.6%; Pred. No. 1.4;  
 Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

OY 1 OYIKANS---KEIGITEL 15  
 Db 14 EYIRNSTVGKFGVGYTEL 31

RESULT 3  
 031590 PRELIMINARY: PRT: 244 AA.  
 AC 031590  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE MHC CLASS II.  
 OS Salmo salar (Atlantic salmon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.  
 NCBI\_TaxID=8030.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSOT-LEUCOCYTES;  
 RA Hotdvalik I., Grimholt U., Fosse V.M., Lie Y., Endresen C.;  
 RL Immunogenetics 0:0-0(0).  
 CC -1- MISCELLANEOUS: FOUND N-TERMINAL TO IMMUNOGLOBULIN AND MAJOR  
 CC HISTOCOMPATIBILITY COMPLEX DOMAIN (BY SIMILARITY).  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 CC -1- SIMILARITY: TO CLASS II HISTOCOMPATIBILITY ANTIGEN, BETA CHAIN.  
 CC BETA-1 DOMAIN INTERPRO FAMILY.  
 DR EMBL: X70166; CAA49725.1;  
 DR InterPro: IPR003597; Ig\_cl.  
 DR InterPro: IPR003066; Ig\_MHC.  
 DR InterPro: IPR000353; MHC\_II\_beta.  
 DR Pfam: PF00047; Ig\_1.  
 DR Pfam: PF00969; MHC\_II\_beta.1.  
 DR ProDom: PD000328; MHC\_II\_beta.1.  
 DR SMART: SM00407; Igcl.1.  
 DR Glycoprotein: MHC; MHC II; Transmembrane.  
 FT NON\_TER 1 71

SO SEQUENCE 244 AA: 27449 MW: 496CB9EA9D73765C CRC64;  
 Query Match 60.1%; Score 44.5; DB 7; Length 244;  
 Best Local Similarity 55.6%; Pred. No. 5;  
 Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

OY 1 OYIKANS---KEIGITEL 15  
 Db 51 EYIRNSTVGKFGVGYTEL 68

RESULT 4  
 09XG37 PRELIMINARY: PRT: 546 AA.  
 AC 09XG37  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DE HYPOTHETICAL 66.2 KDA PROTEIN.  
 OS Guillardia theta (Cryptomonas phi).  
 OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.  
 NCBI\_TaxID=55529;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zauner S., Fraunholz M., Wastl J., Penny S.L., Cavaller-Smith T.,  
 RA Maier U., Douglas S.;  
 RT "Aberrant telomeres, overlapping genes and chloroplast protein-  
 RT encoding functions in an unusually compact eukaryotic genome - the  
 RT cryptomonad nucleomorph."  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ010592; CAB40403.1;  
 DR Hypothetical protein.  
 FT SEQUENCE 546 AA: 66218 MW: 7303950F632BE6F2 CRC64;

Query Match 59.5%; Score 44; DB 10; Length 546;  
 Best Local Similarity 50.0%; Pred. No. 14;  
 Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 2 YIKANSKFIGITEL 15  
 Db 445 FIKSNSRFRRLTEI 458

RESULT 5  
 031578 PRELIMINARY: PRT: 67 AA.  
 AC 031578  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE (DB03) MHC CLASS II BETA 1 (FRAGMENT).  
 OS Salmo salar (Atlantic salmon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.  
 NCBI\_TaxID=8030.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Grimholt U., Olaker I., Vries Lindstrom C., Lie O.;  
 RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.  
 CC -1- MISCELLANEOUS: FOUND N-TERMINAL TO IMMUNOGLOBULIN AND MAJOR  
 CC HISTOCOMPATIBILITY COMPLEX DOMAIN (BY SIMILARITY).  
 CC -1- SIMILARITY: TO CLASS II HISTOCOMPATIBILITY ANTIGEN, BETA CHAIN.  
 CC BETA-1 DOMAIN INTERPRO FAMILY.  
 DR EMBL: L24929; AAA49590.1;  
 DR InterPro: IPR000353; MHC\_II\_beta.  
 DR Pfam: PF00969; MHC\_II\_beta.1.  
 DR ProDom: PD000328; MHC\_II\_beta.1.  
 DR Glycoprotein: MHC; MHC II; Transmembrane.  
 FT NON\_TER 1 67

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 11:15:52 ; Search time 62.77 Seconds  
(without alignments)  
34.954 Million cell updates/sec

Title: US-09-763-397a-24  
Perfect score: 74  
Sequence: 1 QYIKANSKFTGTEL 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP invertebrate:\*  
6: SP mammal:\*  
7: SP mhc:\*  
8: SP organelle:\*  
9: SP phage:\*  
10: SP plant:\*  
11: SP rodent:\*  
12: SP virus:\*  
13: SP vertebrate:\*  
14: SP unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44.5	60.1	60	7	Q31585
2	44.5	60.1	71	7	Q9XRJ9
3	44.5	60.1	244	7	Q31590
4	44	59.5	546	10	Q9XG37
5	43.5	58.8	67	7	Q31578
6	43	58.1	180	2	Q9CF66
7	43	58.1	250	9	Q9MCL7
8	43	58.1	252	9	Q9XUF8
9	43	58.1	302	11	Q9CRV4
10	43	58.1	309	11	Q9CYD2
11	43	58.1	899	12	Q9YTK4
12	42.5	57.4	1087	5	Q25961
13	42.5	57.4	1694	5	Q9NHT1
14	42.5	57.4	1694	5	Q9NHT1
15	42.5	57.4	1704	5	Q9TZW4
16	42.5	57.4	1720	5	Q25922
17	42	56.8	1333	5	Q24262
18	41.5	56.1	84	13	Q9DEK4
19	41.5	56.1	149	7	Q31495

20	41.5	56.1	216	7	Q9GJH0
21	41.5	56.1	216	7	Q9GJH0
22	41	55.4	247	11	Q9B3B9
23	41	55.4	384	4	Q9HD07
24	41	55.4	532	5	Q96671
25	41	55.4	540	5	Q9VU53
26	40.5	54.7	67	7	Q31577
27	40.5	54.7	67	7	Q31581
28	40.5	54.7	67	7	Q31582
29	40.5	54.7	71	7	Q9XRH6
30	40.5	54.7	71	7	Q9XRH1
31	40.5	54.7	84	13	Q9DEJ6
32	40.5	54.7	216	7	Q9GJH2
33	40.5	54.7	217	7	Q9GJH5
34	40.5	54.7	245	7	Q31591
35	40	54.1	134	11	Q9DA16
36	40	54.1	601	2	Q9CEV7
37	39.5	53.4	71	7	Q9XRH4
38	39.5	53.4	131	7	Q46866
39	39.5	53.4	217	7	Q46869
40	39.5	53.4	217	7	Q9GJH7
41	39.5	53.4	217	7	Q9GJH6
42	39	52.7	131	12	Q9YPT2
43	39	52.7	167	4	Q9BYL3
44	39	52.7	304	4	Q9UBP9
45	39	52.7	326	2	Q9ZJ72

## ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	60 AA.
ID Q31585			
AC Q31585			
DT 01-NOV-1996 (TRENBLREL. 01, Created)			
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)			
DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)			
DE (DB02) MHC CLASS II BETA 1 (FRAGMENT).			
OS Salmo salar (Atlantic salmon).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;			
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.			
OX NCBI_TaxID=8030;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Grimholt U., Olsaker I., Vries Lindstrom C., Lie O.,			
RL Submitted (Oct-1993) to the EMBL/GenBank/DBJ databases.			
CC -1- MISCELLANEOUS: FOUND N-TERMINAL TO IMMUNOGLOBULIN AND MAJOR			
CC HISTOCOMPATIBILITY COMPLEX DOMAIN (BY SIMILARITY).			
CC -1- SIMILARITY: TO CLASS II HISTOCOMPATIBILITY ANTIGEN, BETA CHAIN,			
CC BETA-1 DOMAIN INTERPRO FAMILY.			
DR EMBL: L24953; AAA49597.1; .			
DR InterPro: IP000353; MHC_II_beta.			
DR Pfam: PF00969; MHC_II_beta.1.			
DR ProDom: PD000328; MHC_II_beta.1.			
KW Glycoprotein; MHC; MHC II; Transmembrane.			
FT NON_TER 1			
FT NON_TER 60			
FT NON_TER 60			
SQ SEQUENCE 60 AA; 6776 MW; 5D4F3449060940E2 CRC64;			

Query Match 60.1%; Score 44.5; DB 7; Length 60;  
Best Local Similarity 55.6%; Pred. No. 1.2;  
Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY	1 QYIKANSKFTGTEL 15
DB	16 EYIFPNSWTKFVGYTEL 33
RESULT	2
Q9XRJ9	

XX Novel recombinant protein as vaccine for treating malarial infection  
 PT comprises antigenic peptides obtained from different stages of  
 PS plasmodium falciparum life cycle  
 XX Claim 2; Page 16; 52pp; English.  
 CC The present sequence is the antigenic epitope P593, derived from  
 CC circumsporozoite protein (CSP) of the sporozoite stage of Plasmodium  
 CC falciparum. It is used in the construction of recombinant protein  
 CC COC/NIMALVAC-1, which is a multivalent, multistage malarial vaccine.  
 CC The recombinant protein comprises, melittin signal peptide, (His)6 tag,  
 CC T-cell epitope from tetanus toxoid and 21 antigenic epitopes from  
 CC circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2),  
 CC liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1),  
 CC MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175  
 CC (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific  
 CC antigen, Pf27. These epitopes were obtained at different stages of the  
 CC life cycle of P. falciparum. COC/NIMALVAC-1 vaccine has antiparasitic  
 CC activity and can be used for treatment and prevention of malarial  
 CC infections. Anti-COC/NIMALVAC-1 antibodies can be used for detecting  
 CC P. falciparum in biological samples.  
 XX Sequence 23 AA;

Query Match 100.0%; Score 127; DB 21; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-12;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPKDELYENDIEKKICKMEKCS 23  
 |||||  
 DB 1 kpkdelyendiekkickmekcs 23

## RESULT 2

ID AAR66442 standard; peptide; 66 AA.  
 XX AAR66442;  
 AC AAR66442;  
 XX 03-AUG-1995 (first entry)  
 XX Plasmodium falciparum circumsporozoite antigen.  
 XX T cell helper site; cytotoxic T cell response; neutralising antibody;  
 KW P. falciparum CS antigen; circumsporozoite; malaria; vaccine.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FT Region 22..41  
 FT /label= repeat\_region  
 FT /note= "(NANP)5"  
 XX WO9426785-A.  
 XX 24-NOV-1994.  
 XX 13-MAY-1994; 94WO-US05142.  
 XX 14-MAY-1993; 93US-0060988.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX (USSH ) US SEC DEPT HEALTH.  
 XX Ahlers JD, Berzofsky JA, Nara P, Pendleton CD, Shirai M;  
 XX WPI; 1995-006707/01.

XX Polypeptide inducing helper T cell, cytotoxic T cell and  
 PT antibodies responses - to target antigen in hosts of different  
 PT MHC haplotypes, esp. for therapeutic or prophylactic vaccines

PT against HIV.  
 XX Example 4; Page 54; 120pp; English.  
 XX The peptide AAR66442 was synthesised to make a peptide vaccine which  
 CC is recognised by a broad range of MHC types that will elicit a T  
 CC helper cell response, a CTL response and a high titre neutralising  
 CC antibody response.  
 XX Sequence 66 AA;

Query Match 100.0%; Score 127; DB 16; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-11;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPKDELYENDIEKKICKMEKCS 23  
 |||||  
 DB 44 kpkdelyendiekkickmekcs 66

## RESULT 3

ID AAR13175 standard; Protein; 309 AA.  
 XX AAR13175;  
 AC AAR13175;  
 XX 29-AUG-1991 (first entry)  
 XX NS1\_81-RLfdelta9.  
 XX Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;  
 KW hybrid; influenza virus; non-structural protein 1; fusion.  
 XX Plasmodium falciparum.  
 OS Influenza virus (A/PR/8/34/).  
 XX Key Location/Qualifiers  
 FT Region 1..81  
 FT /label= N-terminal of NS1  
 FT /note= "Influenza virus nonstructural protein 1"  
 FT Peptide 82..87  
 FT /label= synthetic linker  
 FT Region 88  
 FT /label= artifact  
 FT /note= "see comments"  
 FT Region 89..193  
 FT /label= AAs 19-123 of CS protein  
 FT /note= "Region I contg. flanking region less  
 FT signal sequence"  
 FT Region 194..309  
 FT /label= AAs 297-412 of CS protein  
 FT /note= "Region II flanking region minus 9 N-term-  
 FT inal AAs"  
 XX EP432965-A.  
 XX 19-JUN-1991.  
 XX 06-DEC-1990; 90EP-0313257.  
 XX 08-DEC-1989; 89US-0447746.  
 XX (SMIK ) SMITHKLINE BEECHAM.  
 XX (USSA ) US SEC OF THE ARMY.  
 XX (BIOM-) BIOMEDICAL RES INST.  
 XX Gross MS, Gordon DM, Hollingdale MR;  
 XX WPI; 1991-179771/25.

XX Polypeptide comprising immunogenic determinants from P falciparum  
 PT - for vaccine against malaria infection in humans.

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OM protein - protein search, using sw model

Run on: January 29, 2002, 10:21:42 ; Search time 310.82 Seconds  
(without alignments)  
5.481 Million cell updates/sec

Title: US-09-763-397A-6

Perfect score: 127

Sequence: 1 KPKDELVDYENDIEKKICKMEKCS 23

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_1101.\*  
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	127	100.0	23	21 AAY70282	Plasmodium falcipa
2	127	100.0	66	16 AAR66442	Plasmodium falcipa
3	127	100.0	309	12 AAR13175	NSI_81-RLfauth9.
4	127	100.0	319	11 AAR07945	NSI81RLfauth plasm
5	127	100.0	319	12 AAR13176	NSI_81-RLfauth. P
6	127	100.0	327	12 AAR13177	NSI_81-RLfauth + (
7	127	100.0	335	12 AAR13178	NSI_81(NANP)ARLFAU
8	127	100.0	335	12 AAR13179	NSI_81(NVDP)ARLFAU
9	127	100.0	350	21 AAY70278	Recombinant vaccin
10	127	100.0	411	9 AAR83144	Sequence encoded b
11	127	100.0	412	7 AAR60416	CS protein of mala

12	127	100.0	424	14 AAR37796	RTS protein. Synt
13	123	96.9	412	9 AAR80835	Sequence encoded b
14	121	95.3	424	14 AAR37797	RTS* protein. Syn
15	120	94.5	180	11 AAR07290	Circumsporozoite a
16	96	75.6	40	16 AAR87213	P.falciparum deriv
17	75	59.1	20	16 AAR71651	CS Region II+ mine
18	71	55.9	21	21 AAY70283	Plasmodium falcipa
19	62	48.8	14	16 AAR71655	Circumsporozoite a
20	62	48.8	19	7 AAP61002	Sequence corresp.
21	60.5	47.6	402	8 AAP70709	Plasmodium cynomol
22	58.5	46.1	19	16 AAR71654	CS Region II+ mine
23	58.5	46.1	168	11 AAR07291	Circumsporozoite a
24	58.5	46.1	272	10 AAP93560	Plasmodium berghei
25	56.5	44.5	478	21 AAB07288	Human II-2/ P. yoe
26	53	41.7	19	21 AAY99033	H1A class II bindi
27	53	41.7	20	22 AAY04118	P.falciparum CS pr
28	53	41.7	21	10 AAR91504	Sequence of modifi
29	53	41.7	21	16 AAR82886	Plasmodium falcipa
30	53	41.7	21	16 AAR78920	Malaria circumspor
31	53	41.7	21	16 AAR75955	P. falciparum CS p
32	53	41.7	21	16 AAR70912	Malaria circumspor
33	53	41.7	21	17 AAW05612	Circumsporozoite h
34	53	41.7	21	18 AAW35440	T-cell stimulatory
35	53	41.7	21	20 AAY23252	Peptide derived fr
36	53	41.7	21	21 AAY80071	Pathogen derived T
37	53	41.7	21	21 AAY54553	T helper cell (Th)
38	53	41.7	21	21 AAY58777	Unidentified pepti
39	53	41.7	21	22 AAG99706	Plasmodium falcipa
40	53	41.7	21	22 AAG62428	Plasmodium falcipa
41	53	41.7	21	22 AAG84517	Plasmodium falcipa
42	53	41.7	21	22 AAG88269	Plasmodium falcipa
43	53	41.7	21	22 AAG89366	Plasmodium falcipa
44	53	41.7	21	22 AAB84447	Sequence of T help
45	53	41.7	21	22 AAB98457	Plasmodium falcipa

## ALIGNMENTS

RESULT 1

AA70282  
ID AAY70282 standard; peptide; 23 AA.

AC AAY70282:

XX 06-JUN-2000 (first entry)

XX Plasmodium falciparum CSP antigenic epitope, P593.

XX Recombinant protein; CDC/NIAIDVAC-1; multivalent; malaria; vaccine;  
KW T-cell epitope; tetanus toxoid; antigenic epitope; treatment; SSP-2;  
KW circumsporozoite protein; CSP; sporozoite surface protein-1; MSP-1;  
KW liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-2;  
KW apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175;  
KW EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen;  
KW Pfg27; antiparasitic; prevention; anti-CDC/NIAIDVAC-1 antibody.

OS Plasmodium falciparum.

XX WO200011179-A1.

XX 02-MAR-2000.

XX 19-AUG-1999; 99WO-US18869.

XX 21-AUG-1998; 98US-0097703.

XX (NAIN-) NAT INST IMMUNOLOGY.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Lal AA, Shi YP, Hasnain SE;

XX WPI; 2000-237654/20.

## Example 2; Page 10; 18pp; English.

PS The polypeptide is prepd. by genetic engineering of genes encoding  
 XX the P. falciparum circumsporozoite (CS) protein [Dame et al.,  
 CC Science 225 : 593 (1984)], and the influenza virus non-structural  
 CC protein 1 (NS1). [Baez et al., Nucleic Acids Research, 8 : 5845  
 CC (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NS1  
 CC (NS1\_81) is linked via a synthetic sequence to DNA encoding Region  
 CC I contg. flanking region less the 18 AA signal region, which in  
 CC turn is fused to DNA encoding Region II-contg. flanking region.  
 CC This CS fusion is designated RLfAuth. The pro residue separating  
 CC the Asp (at the C-terminal of the linker) from RLfAuth is an arti-  
 CC fact of a filled in BamHI site; the Gly separating Region I and  
 CC Region II-contg. CS flanking regions is an artifact of a synthetic  
 CC FokI/ThIII I linker. The peptide can be used in a vaccine for  
 CC protection against malaria.  
 CC The complete nucleotide and AA sequences are given in EP-304720,  
 CC filed May 1, 1990.  
 CC See also AARI2306-R12311 and AARI3175-R13179.

Sequence 319 AA;

Query Match 100.0%; Score 127; DB 12; Length 319;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-10;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPKDELDYENDIEKKICKMEKCS 23  
 |||||  
 DB 275 kpkdelöyendiekkickmekcs 297

## RESULT 6

AARI3177  
 ID AARI3177 standard; Protein; 327 AA.

XX AARI3177;

DT 29-AUG-1991 (first entry)

DE NS1\_81-RLfAuth + (NANP)2.

XX Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;  
 KW hybrid; influenza virus; non-structural protein 1; fusion.

XX Plasmodium falciparum.

OS Influenza virus (A/PR/8/34/).

FH Key Location/Qualifiers

FT Region 1..81 /label= N-terminal of NS1  
 FT /note= "Influenza virus nonstructural protein 1"

FT Peptide 82..87

FT /label= synthetic linker

FT Region 88

FT /label= artifact

FT /note= "see comments"

FT Region 89..193

FT /label= AAs 19-123 of CS protein

FT /note= "Region I contg. flanking region less

FT signal sequence"

FT Region 194..201

FT /label= immunodominant repeat region

FT /note= "two tetrapeptide repeat units"

FT Region 202

FT /label= artifact

FT /note= "see comments"

FT Region 203..327

FT /label= AAs 288-412 of CS protein

FT /note= "Region II flanking region"

XX EP432965-A.

XX

PD 19-JUN-1991.

PF 06-DEC-1990; 90EP-0313257.

PR 08-DEC-1989; 89US-0447746.

XX (SMIK ) SMITHKLINE BEECHAM.

PA (USSA ) US SEC OF THE ARMY.

PA (BIOM-) BIOMEDICAL RES INST.

XX Gross MS, Gordon DM, Hollingdale MR;

XX WPI; 1991-179771/25.

XX Polypeptide comprising immunogenic determinants from P falciparum  
 FT - for vaccine against malaria infection in humans.

XX Example 3; Page 10; 18pp; English.

XX The polypeptide is prepd. by genetic engineering of genes encoding  
 CC the P. falciparum circumsporozoite (CS) protein [Dame et al.,  
 CC Science 225 : 593 (1984)], and the influenza virus non-structural  
 CC protein 1 (NS1). [Baez et al., Nucleic Acids Research, 8 : 5845  
 CC (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NS1  
 CC (NS1\_81) is linked via a synthetic sequence to DNA encoding Region  
 CC I contg. flanking region less the 18 AA signal region. This is  
 CC linked to a synthetic sequence encoding two repeat units from the  
 CC immunodominant region, which in turn is fused to DNA encoding the  
 CC Region II-contg. flanking region. The pro residue separating the  
 CC Asp (at the C-terminal of the linker) from the Region I-contg. CS  
 CC flanking region is an artifact of a filled-in BamHI site; the Gly  
 CC separating the repeat units and the Region II-contg. CS flanking  
 CC region is an artifact of a synthetic FokI/ThIII I linker. The  
 CC peptide can be used in a vaccine for protection against malaria.  
 CC See also AARI2306-R12311 and AARI3175-R13179.

Sequence 327 AA;

Query Match 100.0%; Score 127; DB 12; Length 327;

Best Local Similarity 100.0%; Pred. No. 1.6e-10;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPKDELDYENDIEKKICKMEKCS 23

|||||  
 DB 283 kpkdelöyendiekkickmekcs 305

## RESULT 7

AARI3178

ID AARI3178 standard; Protein; 335 AA.

XX AARI3178;

XX 29-AUG-1991 (first entry)

XX NS1\_81(NANP)4RLfAuth.

XX Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;  
 KW hybrid; influenza virus; non-structural protein 1; fusion.

XX Plasmodium falciparum.

OS Influenza virus (A/PR/8/34/).

FH Key Location/Qualifiers

FT Region 1..81 /label= N-terminal of NS1

FT /note= "Influenza virus nonstructural protein 1"

FT Region 82..97

FT /label= immunodominant repeat region

FT /note= "four tetrapeptide repeat units"

FT Peptide 98..103

FT /label= synthetic linker

XX PS Example 1; Page 7; 18pp; English.

XX CC The polypeptide is prep'd. by genetic engineering of genes encoding  
 CC the P. falciparum circumsporozoite (CS) protein [Dame et al.,  
 CC Science 225 : 593 (1984)], and the influenza-virus non-structural  
 CC protein 1 (NS1), [Baez et al., Nucleic Acids Research, 8 : 5845  
 CC (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NS1  
 CC (NS1-81) is linked via a synthetic sequence to DNA encoding Region  
 CC I contg. flanking region less the 18 AA signal region, which in  
 CC turn is fused to DNA encoding Region II-contg. flanking region  
 CC less the first nine N-terminal AAs. This CS fusion is designated  
 CC RLdelta9. The Pro residue separating the Asp (at the C-terminal  
 CC of the linker) from RLdelta9 is an artifact of a filled in BamHI  
 CC site. The peptide can be used in a vaccine for protection against  
 CC malaria.  
 CC See also AAR12306-R12311 and AAR13176-R13179.

XX SQ Sequence 309 AA;

Query Match 100.0%; Score 127; DB 12; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPKDELDYENDIEKKICKMEKCS 23  
 |||||  
 Db 265 kpkdelyendiekkickmekcs 287

RESULT 4

AAR07945  
 ID AAR07945 standard; protein; 319 AA.

XX AC AAR07945;

DT 22-FEB-1991 (first entry)

XX NS181RLFAuth plasmid product.

XX KW Malaria; vaccine.

XX OS Plasmodium falciparum.

XX FH Key Location/Qualifiers

FT Domain 1..81

FT /label= NS181 protein fragment

FT /note= "from plasmid pMG-1"

FT Domain 89..193

FT /label= Fragment of circumsporozoite protein

FT Domain 204..319

FT /label= Fragment of circumsporozoite protein

XX EP398540-A.

XX PD 22-NOV-1990.

XX PF 01-MAY-1990; 90EP-0304720.

XX PR 03-MAY-1989; 89US-0346863.

XX PA (SMIK ) SMITHKLINE BEECHAM.

XX PI Gross MS, Young JF;

XX WPI: 1990-350299/47.

XX N-PSDB: AAQ06580.

XX New polypeptide used in malaria vaccine - comprises immunogenic

XX determinants from 1st and 2nd flanking regions of plasmodium

XX surface protein and intermediate repeat domain

XX Example 2; Page 11-12; 24pp; English.

PS

XX

CC The product is useful in preparation of vaccines for treatment and  
 CC prophylaxis of plasmodium sporozoite infection. It may be easily  
 CC produced in large pure quantities from a transformed E.coli  
 CC expression system.

XX SQ Sequence 319 AA;

Query Match 100.0%; Score 127; DB 11; Length 319;

Best Local Similarity 100.0%; Pred. No. 1.6e-10;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPKDELDYENDIEKKICKMEKCS 23

|||||  
 Db 275 kpkdelyendiekkickmekcs 297

RESULT 5

AAR13176  
 ID AAR13176 standard; Protein; 319 AA.

XX AC AAR13176;

DT 29-AUG-1991 (first entry)

XX NS1\_81-RLFAuth.

XX Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;

XX KW hybrid; Influenza virus; non-structural protein 1; fusion.

XX OS Plasmodium falciparum.

XX OS Influenza virus (A/PR/8/34).

XX FH Key Location/Qualifiers

FT Region 1..81

FT /label= N-terminal of NS1

FT /note= "Influenza virus nonstructural protein 1"

FT Peptide 82..87

FT /label= synthetic linker

FT Region 88

FT /label= artifact

FT /note= "see comments"

FT Region 89..193

FT /label= AAs 19-123 of CS protein

FT /note= "Region I contg. flanking region less

FT signal sequence"

FT Region 194

FT /label= artifact

FT /note= "see comments"

FT Region 195..319

FT /label= AAs 288-412 of CS protein

FT /note= "Region II flanking region"

XX EP432965-A.

XX PD 19-JUN-1991.

XX PF 06-DEC-1990; 90EP-0313257.

XX PR 08-DEC-1989; 89US-0447746.

XX PA (SMIK ) SMITHKLINE BEECHAM.

XX PI (USSA ) US SEC OF THE ARMY.

XX (BIOM-) BIOMEDICAL RES INST.

XX Gross MS, Gordon DM, Hollingdale MR;

XX WPI: 1991-179771/25.

XX Polypeptide comprising immunogenic determinants from P falciparum

XX - for vaccine against malaria infection in humans.

XX



RC STRAIN-C57BL/6J; TISSUE-EMBRYONIC HEAD;  
RA MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinaagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barsh G.,  
RA Blake J., Bottelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Guenrich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
DR EMBL: AK014093; BAB29151.1; -  
DR MGD: MGI:1920407; 3110030A04Rik.  
DR InterPro: IPR002086; Aldehyde\_dehydr.  
DR Pfam: PF00640; PID: 1.  
DR SMART: SM00462; PTB: 1.  
DR PROSITE: PS00687; ALDEHYDE\_DEHYDR\_GLU; UNKNOWN\_1.  
DR PROSITE: PS01179; PID: 1.  
FT NON\_TER 1 1  
SQ SEQUENCE 302 AA; 34207 MW; 8CB11440F898C65A CRC64;

Query Match 58.1%; Score 43; DB 11; Length 302;  
Best Local Similarity 57.1%; Pred. No. 11;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 YIKANSKFIGITEL 15  
|| 1:11:1 11:  
Db 22 YIPYNAKFLGSTEV 35

RESULT 10  
O9CYD2 PRELIMINARY; PRT; 309 AA.  
AC O9CYD2;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DE 5730529006RIK PROTEIN.  
GN 5730529006RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN 11  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinaagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barsh G.,  
RA Brownstein M.J., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustingich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
DR EMBL: AK017798; BAB30939.1; -  
DR MGD: MGI:1917926; 5730529006RIK.  
DR InterPro: IPR002086; 5730529006RIK.  
DR Pfam: PF00640; PID: 1.  
DR SMART: SM00462; PTB: 1.  
DR PROSITE: PS00687; ALDEHYDE\_DEHYDR\_GLU; UNKNOWN\_1.  
DR PROSITE: PS01179; PID: 1.  
SQ SEQUENCE 309 AA; 35272 MW; 535D8E733C0F406 CRC64;

Query Match 58.1%; Score 43; DB 11; Length 309;  
Best Local Similarity 57.1%; Pred. No. 12;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 YIKANSKFIGITEL 15  
|| 1:11:1 11:  
Db 24 YIPYNAKFLGSTEV 37

RESULT 11  
O9YTK4 PRELIMINARY; PRT; 899 AA.  
AC O9YTK4;  
DT 01-MAY-1999 (TREMBlrel. 10, Created)  
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
DE 01-MAY-1999 (TREMBlrel. 10, Last annotation update)  
DE ORF 63.  
OS Ateline herpesvirus 3.  
OC Vitruvinae; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Gammaherpesvirinae; Rhadinovirus.  
OX NCBI\_TaxID=85618;  
RN 11  
RP SEQUENCE FROM N.A.  
RC STRAIN=73;  
RA Albrecht J.-C., Fleckenstein B.;  
RT "Primary structure of the Herpesvirus Ateles genome.";  
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF083424; AAC95587.1; -  
SQ SEQUENCE 899 AA; 103389 MW; 19440A7944DE2531 CRC64;

Query Match 58.1%; Score 43; DB 12; Length 899;  
Best Local Similarity 64.3%; Pred. No. 36;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 OYKANSKFIGITTE 14  
|| 1:11:1 11:  
Db 124 OYITSSTFGOTE 137

RESULT 12  
O25961 PRELIMINARY; PRT; 1087 AA.  
AC O25961;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE MAJOR SURFACE ANTIGEN (FRAGMENT).  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN 11  
RP SEQUENCE FROM N.A.  
RC STRAIN=RO-71;  
RX MEDLINE=92275047; PubMed=1592091;

SQ SEQUENCE 67 AA; 7449 MW; 42771AEDBABA6626 CRC64;

## Query Match

Best Local Similarity 58.8%; Score 43.5; DB 7; Length 67;  
Matches 9; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

OY 1 QYKANS---KEFIGITEL 15  
: : : : :  
Db 16 EYVRFNSTGKFGVGYTEL 33

## RESULT 6

09CF66 PRELIMINARY; PRT; 180 AA.  
AC 09CF66;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DE SPERMIDINE ACETYLTTRANSFERASE (EC 2.3.1.57).  
GN YQRF.  
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
OX NCBI\_TaxID=1360;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IL1403;  
RA Bolotin A., Wincker P., Manger S., Tallon O., Malarne K.,  
RT Weisenbach J., Ehrlich S.D., Sorokin A.;  
RT "The complete genome sequence of the lactic acid bacterium Lactococcus  
RT lactis.";  
RL Genome Res. 0:0-0(2001).  
DR EMBL; AE006391; AAK05713.1;  
DR InterPro: IPR000182; Acetyltransf\_GCN5.  
DR Pfam: PF00583; Acetyltransf. 1.  
KW Transferase; Complete proteome.  
SQ SEQUENCE 180 AA; 21022 MW; 6DBD148524C0DF3C CRC64;

Query Match 58.1%; Score 43; DB 2; Length 180;  
Best Local Similarity 69.2%; Pred. No. 6.7;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 IKANSKEFIGITEL 15  
: : : : :  
Db 65 IEANDTFIGIVEL 77

## RESULT 7

09MCL7 PRELIMINARY; PRT; 250 AA.  
AC 09MCL7;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
GN ORF13.  
OS Streptococcus thermophilus bacteriophage 7201.  
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.  
OX NCBI\_TaxID=112023;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=20088830; PubMed=10620678;  
RA Stanley E., Walsh L., van der Zwet A., Fitzgerald G.F.,  
RT van Sinderen D.;  
RT "Identification of four loci isolated from two Streptococcus  
RT thermophilus phage genomes responsible for mediating bacteriophage  
RT resistance.";  
RL FEMS Microbiol. Lett. 182:271-277(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Stanley E., Walsh L., Fitzgerald G.F., van Sinderen D.;

RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF145054; AAF43506.1;  
DR InterPro: IPR002295; D2IN6\_mIfase.  
DR InterPro: IPR001091; N6\_Mtase.  
DR InterPro: IPR002941; N6\_Mtase.  
DR Pfam: PF01555; N6\_Mtase; 1.  
DR PRINTS: PR00506; D2IN6MTFRASE.  
DR PRINTS: PR00508; S2IN4MTFRASE.  
SQ SEQUENCE 250 AA; 28744 MW; 725EA3B2B5B0D7F CRC64;

Query Match 58.1%; Score 43; DB 9; Length 250;  
Best Local Similarity 57.1%; Pred. No. 9.5;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 QYKANSKEFIGITE 14  
: : : : :  
Db 131 QVLANMKIVGATE 144

## RESULT 8

09XJEB PRELIMINARY; PRT; 252 AA.  
AC 09XJEB;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DE PUTATIVE TYPE II DNA METHYLTTRANSFERASE.  
OS Lactococcus lactis bacteriophage Tuc2009.  
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.  
OX NCBI\_TaxID=35241;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=99240405; PubMed=10223975;  
RA McGirth S., Seegers J.F., Fitzgerald G.F., van Sinderen D.;  
RT "Molecular characterization of a phage-encoded resistance system in  
RT lactococcus lactis.";  
RL Appl. Environ. Microbiol. 65:1891-1899(1999).  
DR EMBL: AF109874; AAD37103.1;  
DR InterPro: IPR001091; N4\_Mtase.  
DR InterPro: IPR002295; D2IN6\_mIfase.  
DR InterPro: IPR002941; N6\_Mtase.  
DR Pfam: PF01555; N6\_Mtase; 1.  
DR PRINTS: PR00506; D2IN6MTFRASE.  
DR PRINTS: PR00508; S2IN4MTFRASE.  
KW Transferase; Methyltransferase.  
SQ SEQUENCE 252 AA; 29357 MW; 4D5A59FF47363948 CRC64;

Query Match 58.1%; Score 43; DB 9; Length 252;  
Best Local Similarity 57.1%; Pred. No. 9.5;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 QYKANSKEFIGITE 14  
: : : : :  
Db 130 QVLANMKIVGATE 143

## RESULT 9

09CRV4 PRELIMINARY; PRT; 302 AA.  
AC 09CRV4;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DE 3110030A04RIK PROTEIN (FRAGMENT).  
GN 3110030A04RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.

Query Match 100.0%; Score 127; DB 9; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-10;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPRDELVDYNDIEKKICKMEKCS 23  
 DB 367 kpxdelvdyndiekkickmekcs 389

# RESULT 11

AAP60416  
 ID AAP60416 standard; Protein; 412 AA.

AC AAP60416;

DT 13-JUN-1991 (first entry)

DE CS protein of malaria parasite.

XX Sporozoite; vaccination.

OS Plasmodium falciparum.

Key Location/Qualifiers  
 FT Region 124..127  
 FT /label= Repeat unit

PN EPI66410-A.

PD 02-JAN-1986.

PF 24-JUN-1985; 85EP-0107794.

PR 26-JUN-1984; 84US-0624564.

XX (USDC ) US SEC OF COMMERCE.

PA (USGO ) US GOVERNMENT.

PA (USGA ) US SEC OF THE ARMY.

PI McCutchan TF, Dame JB, Williams JL, Schneider I;

DR WPI: 1986-008635/02.

DR N-PSDB: AAN60362.

XX New immunologically active pure synthetic peptide(s) - used for

PT protection against infection by malaria parasite.

PS Disclosure: Fig 2; 49pp; English.

XX The Plasmodium CS gene was used to isolate peptides capable of

CC inducing an immune response to the parasite. Peptide antigens may

CC be synthesised in pure form and used to generate an immune

CC response in vaccination against malaria. The featured repeat

CC units are claimed and must be present in copies of 2-1000.

XX Sequence 412 AA;

Query Match 100.0%; Score 127; DB 7; Length 412;

Best Local Similarity 100.0%; Pred. No. 2.1e-10;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPRDELVDYNDIEKKICKMEKCS 23

DB 368 kpxdelvdyndiekkickmekcs 390

XX 27-SEP-1993 (first entry)

XX RTS protein.

XX RTS; expression cassette; hybrid protein; S. cerevisiae; TDH3;

XX cloning; circumsporozoite protein; CSP; Plasmodium falciparum;

XX strain 7G8; hepatitis B virus; HBV; adv serotype; pres2 protein;

XX S protein.

XX Synthetic.

OS Key

FT Region

FT Region

FT Region

FT Protein

FT Protein

FT Region

FT Region

FT Region

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FT Region

FT Region

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FT Region

FT Region

FT Region

FT Region

1 Location/Qualifiers

2..4 /note= "Derived from S. cerevisiae TDH3 gene sequence"

5..193 /note= "Cloning artefact"

194..197 /note= "Represents amino acids 210-398 of the CSP of P. falciparum"

198..424 /note= "Carboxy terminal amino acids from HBV (adv serotype) pres2 protein"

199..424 /note= "S protein of HBV (adv serotype)"

200..424 /note= "S protein of HBV (adv serotype)"

201..424 /note= "S protein of HBV (adv serotype)"

202..424 /note= "S protein of HBV (adv serotype)"

203..424 /note= "S protein of HBV (adv serotype)"

204..424 /note= "S protein of HBV (adv serotype)"

205..424 /note= "S protein of HBV (adv serotype)"

206..424 /note= "S protein of HBV (adv serotype)"

207..424 /note= "S protein of HBV (adv serotype)"

208..424 /note= "S protein of HBV (adv serotype)"

209..424 /note= "S protein of HBV (adv serotype)"

210..424 /note= "S protein of HBV (adv serotype)"

211..424 /note= "S protein of HBV (adv serotype)"

212..424 /note= "S protein of HBV (adv serotype)"

213..424 /note= "S protein of HBV (adv serotype)"

214..424 /note= "S protein of HBV (adv serotype)"

215..424 /note= "S protein of HBV (adv serotype)"

216..424 /note= "S protein of HBV (adv serotype)"

217..424 /note= "S protein of HBV (adv serotype)"

218..424 /note= "S protein of HBV (adv serotype)"

219..424 /note= "S protein of HBV (adv serotype)"

220..424 /note= "S protein of HBV (adv serotype)"

221..424 /note= "S protein of HBV (adv serotype)"

222..424 /note= "S protein of HBV (adv serotype)"

223..424 /note= "S protein of HBV (adv serotype)"

224..424 /note= "S protein of HBV (adv serotype)"

225..424 /note= "S protein of HBV (adv serotype)"

226..424 /note= "S protein of HBV (adv serotype)"

227..424 /note= "S protein of HBV (adv serotype)"

228..424 /note= "S protein of HBV (adv serotype)"

229..424 /note= "S protein of HBV (adv serotype)"

230..424 /note= "S protein of HBV (adv serotype)"

231..424 /note= "S protein of HBV (adv serotype)"

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252..424 /note= "S protein of HBV (adv serotype)"

253..424 /note= "S protein of HBV (adv serotype)"

254..424 /note= "S protein of HBV (adv serotype)"

255..424 /note= "S protein of HBV (adv serotype)"

256..424 /note= "S protein of HBV (adv serotype)"

257..424 /note= "S protein of HBV (adv serotype)"

258..424 /note= "S protein of HBV (adv serotype)"

259..424 /note= "S protein of HBV (adv serotype)"

260..424 /note= "S protein of HBV (adv serotype)"

261..424 /note= "S protein of HBV (adv serotype)"

262..424 /note= "S protein of HBV (adv serotype)"

263..424 /note= "S protein of HBV (adv serotype)"

264..424 /note= "S protein of HBV (adv serotype)"

265..424 /note= "S protein of HBV (adv serotype)"

266..424 /note= "S protein of HBV (adv serotype)"

267..424 /note= "S protein of HBV (adv serotype)"

268..424 /note= "S protein of HBV (adv serotype)"

269..424 /note= "S protein of HBV (adv serotype)"

270..424 /note= "S protein of HBV (adv serotype)"

271..424 /note= "S protein of HBV (adv serotype)"

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273..424 /note= "S protein of HBV (adv serotype)"

274..424 /note= "S protein of HBV (adv serotype)"

275..424 /note= "S protein of HBV (adv serotype)"

276..424 /note= "S protein of HBV (adv serotype)"

277..424 /note= "S protein of HBV (adv serotype)"

278..424 /note= "S protein of HBV (adv serotype)"

279..424 /note= "S protein of HBV (adv serotype)"

280..424 /note= "S protein of HBV (adv serotype)"

281..424 /note= "S protein of HBV (adv serotype)"

282..424 /note= "S protein of HBV (adv serotype)"

283..424 /note= "S protein of HBV (adv serotype)"

284..424 /note= "S protein of HBV (adv serotype)"

285..424 /note= "S protein of HBV (adv serotype)"

286..424 /note= "S protein of HBV (adv serotype)"

287..424 /note= "S protein of HBV (adv serotype)"

288..424 /note= "S protein of HBV (adv serotype)"

289..424 /note= "S protein of HBV (adv serotype)"

290..424 /note= "S protein of HBV (adv serotype)"

291..424 /note= "S protein of HBV (adv serotype)"

292..424 /note= "S protein of HBV (adv serotype)"

293..424 /note= "S protein of HBV (adv serotype)"

294..424 /note= "S protein of HBV (adv serotype)"

295..424 /note= "S protein of HBV (adv serotype)"

296..424 /note= "S protein of HBV (adv serotype)"

297..424 /note= "S protein of HBV (adv serotype)"

298..424 /note= "S protein of HBV (adv serotype)"

299..424 /note= "S protein of HBV (adv serotype)"

300..424 /note= "S protein of HBV (adv serotype)"

301..424 /note= "S protein of HBV (adv serotype)"

302..424 /note= "S protein of HBV (adv serotype)"

303..424 /note= "S protein of HBV (adv serotype)"

304..424 /note= "S protein of HBV (adv serotype)"

305..424 /note= "S protein of HBV (adv serotype)"

306..424 /note= "S protein of HBV (adv serotype)"

307..424 /note= "S protein of HBV (adv serotype)"

308..424 /note= "S protein of HBV (adv serotype)"

309..424 /note= "S protein of HBV (adv serotype)"

310..424 /note= "S protein of HBV (adv serotype)"

311..424 /note= "S protein of HBV (adv serotype)"

312..424 /note= "S protein of HBV (adv serotype)"

313..424 /note= "S protein of HBV (adv serotype)"

314..424 /note= "S protein of HBV (adv serotype)"

315..424 /note= "S protein of HBV (adv serotype)"

316..424 /note= "S protein of HBV (adv serotype)"

317..424 /note= "S protein of HBV (adv serotype)"

318..424 /note= "S protein of HBV (adv serotype)"

319..424 /note= "S protein of HBV (adv serotype)"

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343..424 /note= "S protein of HBV (adv serotype)"

344..424 /note= "S protein of HBV (adv serotype)"

345..424 /note= "S protein of HBV (adv serotype)"

346..424 /note= "S protein of HBV (adv serotype)"

347..424 /note= "S protein of HBV (adv serotype)"

348..424 /note= "S protein of HBV (adv serotype)"

349..424

DB 163 kpkdeldyendiekkickmekcs 185

### RESULT 13

ID AAP80835 standard: protein; 412 AA.

XX AAP80835;

DT 18-SEP-1990 (first entry)

DE Sequence encoded by the circumsporozoite (CS) gene of Plasmodium falciparum in lambda mpfl.

XX Circumsporozoite gene: Plasmodium falciparum; lambda mpfl; vaccine;  
KM yeast glyceraldehyde-3P-dehydrogenase gene (TDH3) promoter;  
KM yeast ornithine carbamoyl transferase gene (ARG3); repeat region.

OS Plasmodium falciparum

XX Key Location/Qualifiers

FT Region 124..147 /note="repeat region, repeat unit=NNPNVDP"

FT Region 148..207 /note="repeat region, repeat unit=NNNP"

FT Region 212..287 /note="repeat region, repeat unit=NNNP"

FT WO8805817-A.

PN 11-SEP-1988.

PD 25-JAN-1988; 88WO-BE00002.

PF 30-JAN-1987; 87US-0008791.

PR (SMIK) SMITH KLINE RIT SA.

PA De Wilde M, Gathoye AM;

PI WPI; 1988-235171/33.

DR N-PSDB; AAN81781.

XX Expression of P. falciparum circumsporozoite protein by yeast -  
PT using recombinant DNA vector having coding sequence linked to  
PT expression control sequence

XX Example 1; Fig 2a; 44pp; English.

XX Plasmid WR201 was obtained from the Walter Reed Army Institute of  
CC Research, and results from insertion of a 2.3 kb EcoRI fragment from  
CC lambda mpfl encoding the complete CS protein gene P. falciparum into  
CC vector pUC8. A recombinant DNA vector is claimed, which comprises a DNA  
CC sequence contg. the coding sequence of the CS P. falciparum operatively  
CC linked to an expression control sequence. Pfief. expression control  
CC sequences include the yeast glyceraldehyde-3P-dehydrogenase gene (TDH3)  
CC promoter and the yeast ornithine carbamoyl transferase gene (ARG3)  
CC transcription termination region. A suitable coding sequence comprises  
CC the 1215bp StuI-RsaI fragment of WR201 contg. the P. falciparum CS  
CC protein coding sequence, minus its first 50bp. Also claimed is a  
CC transformed host cell, a method of culturing the cell to produce CS, the  
CC protein, and a vaccine. The vector comprises a 192 bp Sau3A fragment  
CC coding for 16 tetrapeptide repeats of the P. falciparum CS protein  
CC derived from Sau3A digestion of a 1215 bp StuI-RsaI fragment of WR201  
CC containing the P. falciparum CS protein coding sequence minus  
CC approx. its first 50 bp, or two, three, four or more tandem copies of  
CC such 192 bp Sau3A fragment.

XX Sequence 412 AA;

Query Match 96.9%; Score 123  
Best-Local Similarity 95.7%; Pred. No.

Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPRDELDYENDIEKKICKMEKCS 23

DB 368 kpkdeldyendiekkickmekcs 390

### RESULT 14

ID AAR37797 standard: Protein; 424 AA.

XX AAR37797;

DT 27-SEP-1993 (first entry)

DE RTS\* protein.

XX RTS; expression cassette; hybrid protein; S. cerevisiae; TDH3;

KM cloning; circumsporozoite protein; CSP; Plasmodium falciparum;

KM strain 7G8; hepatitis B virus; HBV; adv serotype; pres2 protein;

XX S protein.

XX Synthetic.

OS Key Location/Qualifiers

FT Region 1 /note="Derived from S. cerevisiae TDH3 gene sequence"

FT Region 2..4 /note="Cloning artefact"

FT Protein 5..193 /note="Represents amino acids 210-398 of the CSP of P. falciparum"

FT Region 194..197 /note="Carboxy terminal amino acids from HBV (adv serotype) pres2 protein"

FT Protein 198..424 /note="S protein of HBV (adv serotype)"

PN WO9310152-A.

PD 27-MAY-1993.

PF 11-NOV-1992; 92WO-EP02591.

PR 16-NOV-1991; 91GB-0024390.

PR 27-FEB-1992; 92US-0842694.

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

PI Cohen J, De Wilde M;

DR WPI; 1993-182494/22.

DR N-PSDB; AAG42567.

XX Hybrid protein comprising Plasmodium circumsporozoite protein and  
PT HbsAg - useful as a vaccine for treating patients susceptible to  
PT Plasmodium infections

XX Disclosure; Fig 9; 59pp; English.

XX This sequence represents the RTS\* hybrid protein which is encoded by  
CC the RTS\* expression cassette. This hybrid consists of a methionine  
CC residue derived from S. cerevisiae TDH3 gene sequence, three amino  
CC acids, Met-Ala-Pro, derived from a nucleotide sequence created by  
CC the cloning procedure used to construct the hybrid gene, a stretch  
CC of 189 amino acids representing amino acids 210 to 398 of the  
CC circumsporozoite protein (CSP) of Plasmodium falciparum strain NF54,  
CC an amino acid Arg created by the cloning procedure, four amino acids,  
CC Pro-Val-Thr-Asn, representing the four carboxy terminal residues of  
CC hepatitis B virus (HBV), adv serotype, pres2 protein, and a stretch  
CC of 226 amino acids specifying the S protein of HBV, adv serotype.  
CC This protein, and RTS (see also AAR37796), may be combined with an  
CC adjuvant and used in a vaccine for preventing Plasmodium infections.

Job time: 419 sec

CC The vaccines produce a humoral response and also a cellular immune  
CC response.  
XX  
SQ Sequence 424 AA;

Query Match 95.3%; Score 121; DB 14; Length 424;  
Best Local Similarity 95.7%; Pred. No. 1.6e-09;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPKDELDYENDIEKKICKMEKCS 23  
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Db 159 kpkdeldyendiekkickmekcs 181

RESULT 15

AA07290  
ID AA07290 standard; protein; 180 AA.

AC AA07290;

DT 28-JAN-1991 (first entry)

DE Circumsporozoite analogue Falci-parum 4.

KW CS protein; plasmodium; malaria; vaccine.

OS Synthetic.

PN EP392820-A.

PD 17-OCT-1990.

PF 11-APR-1990; 90EP-0303907.

PR 11-APR-1989; 89US-0336288.

PA (CHIR-) CHIRON CORP.

PI Barr PJ, Bathurst IC, Gibson HL;

DR WPI; 1990-314486/42.

N-PSDB; AA06153.

PT Recombinant Plasmodium circumsporozoite analogues - lacking  
PT one or more repeat epitope(s) for use as a malaria sub-unit  
PT vaccine.

PS Claim 10; Fig 10; 22pp; English.

CC The protein was produced by expression of a synthetic gene. The  
CC analogue comprises AAs 68-123 of the native P. falciparum CS  
CC protein, followed by four repeat sequences (three "B"s, i.e. MANP)  
CC and one "A", i.e. NYDP), followed by AAs 289-392 of the native  
CC protein. Reduction of the immunological dominance of the repeats  
CC relative to the epitopes in the regions flanking the repeats  
CC enhances sporozoite neutralising activity.  
CC See also AA07287-91.

SQ Sequence 180 AA;

Query Match 94.5%; Score 120; DB 11; Length 180;  
Best Local Similarity 95.7%; Pred. No. 8.6e-10;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPKDELDYENDIEKKICKMEKCS 23  
|||||  
Db 157 kpkdeldyendiekkickmekcs 179



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 10:24:02 ; Search time 133.18 Seconds  
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3.886 Million cell updates/sec

Title: US-09-763-397A-6

Perfect score: 127

Sequence: 1 KPKDELVDYENDIEKRIKMEKCS 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/2/1aa/5A-COMB.pep:\*

2: /cgn2\_6/ptodata/2/1aa/5B-COMB.pep:\*

3: /cgn2\_6/ptodata/2/1aa/5A-COMB.pep:\*

4: /cgn2\_6/ptodata/2/1aa/5B-COMB.pep:\*

5: /cgn2\_6/ptodata/2/1aa/5A-COMB.pep:\*

6: /cgn2\_6/ptodata/2/1aa/5B-COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	127	100.0	66	2	US-08-455-625-35
2	127	100.0	66	4	US-08-455-685-35
3	127	100.0	66	4	US-08-060-988A-35
4	127	100.0	66	5	PCT-US94-05142-35
5	127	100.0	412	1	US-08-313-288B-18
6	127	100.0	423	2	US-08-760-797A-1
7	127	100.0	424	2	US-08-932-929B-1
8	121	95.3	424	4	US-08-760-797A-3
9	121	95.3	424	4	US-08-932-929B-3
10	85	66.9	32	6	517861-7
11	85	66.9	32	6	517861-7
12	75	64.6	15	2	US-08-318-856A-75
13	75	64.6	15	2	US-08-318-856A-75
14	56.5	59.1	19	6	517861-18
15	56.5	59.1	19	6	517861-18
16	53	41.7	21	1	US-08-186-266-6
17	53	41.7	21	1	US-08-446-692-48
18	53	41.7	21	2	US-08-446-692-48
19	53	41.7	21	2	US-08-446-692-48
20	53	41.7	21	5	US-09-100-409A-54
21	53	41.7	21	5	PCT-US95-02121-97
22	53	41.7	33	2	US-08-446-692-27
23	53	41.7	33	2	US-08-446-692-27
24	50	39.4	9	2	US-08-488-351A-27
25	47	37.0	9	2	517843-9
26	47	37.0	9	2	US-08-318-856A-20
27	46.5	36.6	4	4	US-08-215-221-25
					US-08-845-258-21

28	46.5	36.6	492	4	US-08-990-571-21	Sequence 21, Appl
29	46.5	36.6	492	4	US-08-723-142A-21	Sequence 21, Appl
30	46.5	36.6	503	4	US-08-845-258-52	Sequence 52, Appl
31	46.5	36.6	503	4	US-08-990-571-52	Sequence 52, Appl
32	46	36.2	863	4	US-09-238-303-11	Sequence 11, Appl
33	45	35.4	8	2	US-08-318-856A-1	Sequence 1, Appl
34	45	35.4	8	2	PCT-US95-02121-17	Sequence 17, Appl
35	45	35.4	9	2	US-08-318-856A-27	Sequence 27, Appl
36	44	34.6	607	2	US-08-472-534-5	Sequence 5, Appl
37	44	34.6	714	2	US-08-472-534-3	Sequence 3, Appl
38	44	34.6	1400	1	US-08-080-255-7	Sequence 7, Appl
39	44	34.6	1400	3	US-08-465-713-7	Sequence 7, Appl
40	44	34.6	1400	5	PCT-US93-05857-7	Sequence 7, Appl
41	44	34.6	3969	4	US-08-061-376-5	Sequence 5, Appl
42	43.5	34.3	1264	1	US-07-789-915A-6	Sequence 6, Appl
43	43.5	34.3	1264	1	US-08-005-002C-6	Sequence 6, Appl
44	43.5	34.3	1264	1	US-08-487-203A-6	Sequence 6, Appl
45	43	33.9	16	2	US-08-817-933A-7	Sequence 7, Appl

## ALIGNMENTS

RESULT 1  
US-08-455-625-35  
Sequence 35, Application US/08455625  
Patent No. 5932218  
GENERAL INFORMATION:  
APPLICANT: Berzofsky, Jay A.  
APPLICANT: Ahlers, Jeffrey D.  
APPLICANT: Pendleton, C. D.  
APPLICANT: Nara, Peter  
TITLE OF INVENTION: COMPOSITE SYNTHETIC PEPTIDE CONSTRUCT  
TITLE OF INVENTION: ELICITING NEUTRALIZING ANTIBODIES AND CYTOTOXIC T  
NUMBER OF INVENTION: LYMPHOCYTES AGAINST HIV  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch & Birch  
STREET: P.O. Box 747  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,625  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/060,988  
FILING DATE: 14-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.  
REGISTRATION NUMBER: 30330  
REFERENCE/DOCKET NUMBER: 1173-434P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-205-8000  
TELEFAX: 703-205-8050  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 66 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLCULE TYPE: peptide  
FRAGMENT TYPE: Internal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..66

OTHER INFORMATION: /label= peptide  
OTHER INFORMATION: /note= "peptide from P. falciparum CS antigen"  
US-08-455-625-35

Query Match 100.0%; Score 127; DB 2; Length 66;  
Best Local Similarity 100.0%; Pred. No. 8,9e-12;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPKDELDYENDIEKKICKMEKCS 23  
Db 44 KPKDELDYENDIEKKICKMEKCS 66

## RESULT 2

US-08-455-685-35  
Sequence 35, Application US/08455685  
Patent No. 6214347  
GENERAL INFORMATION:  
APPLICANT: Berzofsky, Jay A.  
APPLICANT: Ahlers, Jeffrey D.  
APPLICANT: Pendleton, C. David  
APPLICANT: Nara, Peter  
APPLICANT: Shirai, Mutsunori  
TITLE OF INVENTION: MULTIDETERMINANT PEPTIDES THAT ELICIT  
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND  
TITLE OF INVENTION: NEUTRALIZING ANTIBODY RESPONSES AGAINST HIV-1  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,685  
FILING DATE: 31-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/060,988  
FILING DATE: 14-MAY-1993  
APPLICATION NUMBER: 07/847,311  
FILING DATE: 06-MAR-1992  
APPLICATION NUMBER: 07/751,998  
FILING DATE: 29-AUG-1991  
APPLICATION NUMBER: 07/148,692  
FILING DATE: 26-JAN-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Beattie, Ingrid A.  
REGISTRATION NUMBER: P-42,306  
REFERENCE/DOCKET NUMBER: 08830/022003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 66 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-455-685-35

Query Match 100.0%; Score 127; DB 4; Length 66;  
Best Local Similarity 100.0%; Pred. No. 8,9e-12;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPKDELDYENDIEKKICKMEKCS 23  
Db 44 KPKDELDYENDIEKKICKMEKCS 66

## RESULT 3

US-08-060-988A-35  
Sequence 35, Application US/08060988A  
Patent No. 6294322  
GENERAL INFORMATION:  
APPLICANT: Berzofsky, Jay A.  
APPLICANT: Ahlers, Jeffrey D.  
APPLICANT: Pendleton, C. David  
APPLICANT: Nara, Peter  
APPLICANT: Shirai, Mutsunori  
TITLE OF INVENTION: MULTIDETERMINANT PEPTIDES  
TITLE OF INVENTION: THAT ELICIT  
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND  
TITLE OF INVENTION: NEUTRALIZING ANTIBODY RESPONSES AGAINST HIV-1  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/060,988A  
FILING DATE: 14-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/847,311  
FILING DATE: 06-MAR-1992  
APPLICATION NUMBER: 07/751,998  
FILING DATE: 29-AUG-1991  
APPLICATION NUMBER: 07/148,692  
FILING DATE: 26-JAN-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Beattie, Ingrid A.  
REGISTRATION NUMBER: P-42,306  
REFERENCE/DOCKET NUMBER: 08830/022001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 66 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-060-988A-35

Query Match 100.0%; Score 127; DB 4; Length 66;  
Best Local Similarity 100.0%; Pred. No. 8,9e-12;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPKDELDYENDIEKKICKMEKCS 23  
Db 44 KPKDELDYENDIEKKICKMEKCS 66

## RESULT 4

PCT-US94-05142-35  
Sequence 35, Application PC/TUS9405142  
GENERAL INFORMATION:  
APPLICANT:



;; TITLE OF INVENTION: COMPOSITE SYNTHETIC PEPTIDE CONSTRUCT  
;; TITLE OF INVENTION: ELICITING NEUTRALIZING ANTIBODIES AND CYTOTOXIC T  
;; TITLE OF INVENTION: LYMPHOCYTES AGAINST HIV  
;; NUMBER OF SEQUENCES: 36  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Birch, Stewart, Kolasch & Birch  
;; STREET: P.O. Box 747  
;; CITY: Falls Church  
;; STATE: Virginia  
;; COUNTRY: USA  
;; ZIP: 22040-0747  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US94/05142  
;; FILING DATE: 13-MAY-1994  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/060,988  
;; FILING DATE: 14-MAY-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Svensson, Leonard R.  
;; REGISTRATION NUMBER: 30330  
;; REFERENCE/DOCKET NUMBER: 1173-434P  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 703-205-8000  
;; TELEFAX: 703-205-8050  
;; INFORMATION FOR SEQ ID NO: 35:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 66 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FRAGMENT TYPE: internal  
;; FEATURE:  
;; NAME/KEY: Peptide  
;; LOCATION: 1..66  
;; OTHER INFORMATION: /label= peptide  
;; OTHER INFORMATION: /note= "peptide from P. falciparum CS antigen"  
PCT-US94-05142-35  
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;; Best Local Similarity 100.0%; Pred. No. 8.9e-12;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 KPDELVDYNDIEKKICKMKCS 23  
Db 44 KPDELVDYNDIEKKICKMKCS 66  
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RESULT 5  
US-08-313-288B-18  
;; Sequence 18, Application US/08313288B  
;; Patent No. 5750502  
;; GENERAL INFORMATION:  
;; APPLICANT: Jessell, Thomas M. and Avihu Klar  
;; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A  
;; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPOINDIN  
;; NUMBER OF SEQUENCES: 20  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Cooper & Dunham LLP  
;; STREET: 1185 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10036  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/313,288B  
;; FILING DATE: January 5, 1995  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: White, John P.  
;; REGISTRATION NUMBER: 28,678  
;; REFERENCE/DOCKET NUMBER: 40028-A-PCT-US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 278-0400  
;; TELEFAX: (212) 391-0526  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 18:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 412 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-313-288B-18  
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;; Query Match 100.0%; Score 127; DB 1; Length 412;  
;; Best Local Similarity 100.0%; Pred. No. 6.3e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 KPDELVDYNDIEKKICKMKCS 23  
Db 368 KPDELVDYNDIEKKICKMKCS 390  
;;

RESULT 6  
US-08-760-797A-1  
;; Sequence 1, Application US/08760797A  
;; Patent No. 5928902  
;; GENERAL INFORMATION:  
;; APPLICANT: De Wilde, Michel  
;; APPLICANT: Cohen, Joseph  
;; TITLE OF INVENTION: Hybrid Protein Between CS  
;; TITLE OF INVENTION: from Plasmodium and HBsAg  
;; NUMBER OF SEQUENCES: 4  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: SmithKline Beecham Corporation  
;; STREET: 709 Swedeland Road  
;; CITY: King of Prussia  
;; STATE: PA  
;; COUNTRY: USA  
;; ZIP: 19406  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/760,797A  
;; FILING DATE: 04-DEC-1996  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/442,612  
;; FILING DATE: 17-MAY-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Baumeister, Kirk  
;; REGISTRATION NUMBER: 33,833  
;; REFERENCE/DOCKET NUMBER: B45015-1C2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 610-270-5096  
;; TELEFAX: 610-270-5090  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 423 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-760-797A-1

Query Match 100.0%; Score 127; DB 2; Length 423;  
Best Local Similarity 100.0%; Pred. No. 6.5e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPKDELVDYNDIEKKICKMEKCS 23  
DB 162 KPKDELVDYNDIEKKICKMEKCS 184

RESULT 7  
US-08-932-929B-1  
Sequence 1, Application US/08932929B  
Patent No. 6169171  
GENERAL INFORMATION:  
APPLICANT: De Wilde, Michel  
APPLICANT: Cohen, Joseph  
TITLE OF INVENTION: Hybrid Protein Between CS  
TITLE OF INVENTION: from Plasmidium and HBSAG  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/932,929B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/760,797  
FILING DATE: 04-DEC-1996  
APPLICATION NUMBER: 08/442,612  
FILING DATE: 17-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk  
REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: B45015-1FWC2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 424 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-932-929B-1

Query Match 100.0%; Score 127; DB 4; Length 424;  
Best Local Similarity 100.0%; Pred. No. 6.5e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPKDELVDYNDIEKKICKMEKCS 23  
DB 163 KPKDELVDYNDIEKKICKMEKCS 185

RESULT 8

US-08-760-797A-3  
Sequence 3, Application US/08760797A  
Patent No. 5928902

GENERAL INFORMATION:  
APPLICANT: De Wilde, Michel  
APPLICANT: Cohen, Joseph  
TITLE OF INVENTION: Hybrid Protein Between CS  
TITLE OF INVENTION: from Plasmidium and HBSAG  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/760,797A

FILING DATE: 04-DEC-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/442,612

FILING DATE: 17-MAY-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk

REGISTRATION NUMBER: 33,833

REFERENCE/DOCKET NUMBER: B45015-1C2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096

TELEFAX: 610-270-5090

TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 424 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-760-797A-3

Query Match 95.3%; Score 121; DB 2; Length 424;  
Best Local Similarity 95.7%; Pred. No. 4.8e-10;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPKDELVDYNDIEKKICKMEKCS 23  
DB 159 KPKDELVDYNDIEKKICKMEKCS 181

RESULT 9

US-08-932-929B-3  
Sequence 3, Application US/08932929B  
Patent No. 6169171

GENERAL INFORMATION:  
APPLICANT: De Wilde, Michel

APPLICANT: Cohen, Joseph

TITLE OF INVENTION: Hybrid Protein Between CS  
TITLE OF INVENTION: from Plasmidium and HBSAG  
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/932,929B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/760,797  
FILING DATE: 04-DEC-1996  
APPLICATION NUMBER: 08/442,612  
FILING DATE: 17-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk  
REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: B45015-1FWC2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 424 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-932-929B-3

Query Match 95.3%; Score 121; DB 4; Length 424;  
Best Local Similarity 95.7%; Pred. No. 4.8e-10;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KRPDELVDYNDIEKKICKMEKCS 23  
DB 159 KRPDELVDYNDIEKKICKMEKCS 181

RESULT 10  
517861-7  
PATENT NO. 517861  
APPLICANT: VERGARA, ULISES; RUIZ, ANDRES; FERREIRA, ARTURO;  
NUSSENZWEIG, RUTH S.; NUSSENZWEIG, VICTOR N.  
TITLE OF INVENTION: CROSS-REACTIVE AND PROTECTIVE EPITOPES  
OF CIRCUMPOROZOITE PROTEINS  
NUMBER OF SEQUENCES: 18  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/370,241  
FILING DATE: 22-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 115,634  
FILING DATE: 26-OCT-1987  
APPLICATION NUMBER: 649,903  
FILING DATE: 12-SEP-1984  
SEQ ID NO: 7  
LENGTH: 32  
517861-7

Query Match 66.9%; Score 85; DB 6; Length 32;  
Best Local Similarity 94.1%; Pred. No. 4.8e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KRPDELVDYNDIEKKIC 17  
DB 16 KRPDELVDYNDIEKKIC 32

RESULT 11  
US-08-318-856A-75  
SEQUENCE 75, Application US/0831856A  
PATENT NO. 5972351  
GENERAL INFORMATION:

APPLICANT: Adrian V.S. Hill, et al.  
TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-  
TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE  
TITLE OF INVENTION: ANTIGENS (AS AMENDED)  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., Suite 800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1+  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/318,856A  
FILING DATE: October 3, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 92 08 068.8  
FILING DATE: April 3, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 92 17 704.7  
FILING DATE: August 20, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/GB93/00711  
FILING DATE: April 5, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee Cheng  
REGISTRATION NUMBER: 40,949  
REFERENCE/DOCKET NUMBER: 263-PP1R15770S  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 721-8200  
TELEFAX: (202) 721-8250  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acid residues  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-318-856A-75

Query Match 64.6%; Score 82; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 ENDIEKKICKMEKCS 23  
DB 1 ENDIEKKICKMEKCS 15

RESULT 12  
US-08-318-856A-76  
SEQUENCE 76, Application US/0831856A  
PATENT NO. 5972351  
GENERAL INFORMATION:  
APPLICANT: Adrian V.S. Hill, et al.  
TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-  
TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE  
TITLE OF INVENTION: ANTIGENS (AS AMENDED)  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., Suite 800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1+  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/318,856A  
FILING DATE: October 3, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 92 08 068.8  
FILING DATE: April 3, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 92 17 704.7  
FILING DATE: August 20, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/GB93/00711  
FILING DATE: April 5, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee Cheng  
REGISTRATION NUMBER: 40,949  
REFERENCE/DOCKET NUMBER: 263-PIR1577US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (702) 721-8200  
TELEFAX: (202) 721-8250  
INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acid residues  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-318-856A-76

Query Match 59.1%; Score 75; DB 2; Length 15;  
Best Local Similarity 93.3%; Pred. No. 5.9e-05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ELDYNDIEKKICKM 19  
DB 1 ELDYNDIEKKICKM 15

RESULT 13  
5178861-18  
PATENT NO. 5178861  
APPLICANT: VERGARA, ULISES; RUIZ, ANDRES; FERREIRA, ARTURO;  
NUSSENZWEIG, KUTH S.; NUSSENZWEIG, VICTOR N.  
TITLE OF INVENTION: CROSS-REACTIVE AND PROTECTIVE EPITOPES  
OF CIRCUMFEROZOITE PROTEINS  
NUMBER OF SEQUENCES: 18  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/370,241  
FILING DATE: 22-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 115,634  
FILING DATE: 26-OCT-1987  
APPLICATION NUMBER: 649,903  
FILING DATE: 12-SEP-1984  
SEQ ID NO: 18  
LENGTH: 19  
5178861-18

Query Match 44.9%; Score 57; DB 6; Length 19;  
Best Local Similarity 91.7%; Pred. No. 0.031;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPKDELIDYNDI 12  
DB 7 KPKDELIDYNDI 18

RESULT 14

US-08-155-888-2  
Sequence 2, Application US/08155888  
Patent No. 6066623  
GENERAL INFORMATION:  
APPLICANT: Hoffman, Stephen L.  
APPLICANT: Hedstrom, Richard C.  
APPLICANT: Sedegah, Martha  
TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE PROTECTIVE  
AGAINST MALARIA, METHODS OF PROTECTION AND VECTOR FOR  
DELIVERING POLYNUCLEOTIDE VACCINES  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Naval Medical Res. & Dev. Cnd.  
STREET: Bldg. 1, T-12 8901 Wisconsin Ave.  
CITY: Bethesda  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20889-5606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/155,888  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Spevack, A. David  
REGISTRATION NUMBER: 24,743  
REFERENCE/DOCKET NUMBER: N.C. 75,851  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 295-1022  
TELEFAX: (202) 295-6759  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 478 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-155-888-2

Query Match 44.5%; Score 56.5; DB 3; Length 478;  
Best Local Similarity 52.2%; Pred. No. 1.1;  
Matches 12; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 KPKDELIDYNDIEKKICKMEKCS 23  
DB 435 KPEPNTLE-DIDYELCKMDKCS 456

RESULT 15  
US-08-186-266-6  
Sequence 6, Application US/08186266  
Patent No. 5662907  
GENERAL INFORMATION:  
APPLICANT: KUHO, Ralph T.  
APPLICANT: GREY, Howard M.  
APPLICANT: SETTY, Alessandro  
APPLICANT: CELIS, Estden  
TITLE OF INVENTION: INDUCTION OF ANTI-TUMOR CYTOTOXIC  
TITLE OF INVENTION: T LYMPHOCYTES IN HUMANS USING  
SYNTHETIC PEPTIDE EPITOPES  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourile and Crew  
STREET: Stewart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:

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: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/186,266
: FILING DATE: 25-JAN-1994
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/159,339
: FILING DATE: 29-NOV-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/103,396
: FILING DATE: 06-AUG-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/027,746
: FILING DATE: 05-MAR-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/926,666
: FILING DATE: 07-AUG-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Bastian, Kevin L.
: REGISTRATION NUMBER: 34,774
: REFERENCE/DOCKET NUMBER: 14137-50-4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 543-9600
: TELEFAX: (415) 543-5043
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 21 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Peptide
: LOCATION: 1..21
: OTHER INFORMATION: /note="Plasmodium falciparum CS
: OTHER INFORMATION: protein at positions 378-398."
: US-08-186-266-6

```

```

Query Match 41.7%; Score 53; DB 1; Length 21;
Best Local Similarity 84.6%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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```

OY 11 DIEKKICKMEKCS 23
    ||||| |||||
Db 1 DIEKKIAKMEKAS 13

```

Search completed: January 29, 2002, 10:24:03  
 Job time: 509 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 29, 2002, 10:26:36 ; Search time 144.96 Seconds  
(without alignments)  
12.086 Million cell updates/sec

Title: US-09-763-397A-6

Perfect score: 127  
Sequence: 1 KPKDELVDYENDIEKKICKMEKCS 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	100.0	412	1	OZQOAF
2	127	100.0	424	1	A54533
3	124	97.6	442	2	A54529
4	122	96.1	388	2	A3756
5	121	95.3	405	2	S05428
6	71	55.9	38	2	C60657
7	68	53.5	38	2	D60657
8	68	53.5	38	2	E60657
9	65	51.2	38	2	A38869
10	65	51.2	38	2	B60657
11	63	49.6	38	2	H60657
12	63	49.6	38	2	B38869
13	62	48.8	38	2	G60657
14	62	48.8	38	2	F60657
15	62	48.8	189	2	B29795
16	61.5	48.4	388	2	JC6164
17	60.5	47.6	378	1	OZQOAB
18	60.5	47.6	378	1	OZQOAL
19	60.5	47.6	398	1	OZQOAS
20	60.5	47.6	401	1	OZQOAM
21	60.5	47.6	419	1	OZQOAN
22	58.5	46.1	332	1	OZQOMB
23	58.5	46.1	348	1	OZQOKB
24	56.5	44.5	264	1	A44969
25	56.5	44.5	367	1	OZQOMY
26	53	41.7	177	2	S57043
27	51	40.2	343	2	A29319
28	51	40.2	367	2	A32068
29	51	40.2	378	1	OZQOAV

30	51	40.2	386	2	A48571	circumsporozoite p
31	51	40.2	387	2	D41156	circumsporozoite p
32	51	40.2	387	2	C41156	circumsporozoite p
33	51	40.2	395	2	A41156	circumsporozoite p
34	49.5	39.0	993	2	B64695	type I restriction
35	49	38.6	387	2	B82891	ferichrome transp
36	49	38.6	429	2	A54504	circumsporozoite p
37	49	38.6	485	2	A60610	circumsporozoite p
38	49	38.6	802	2	T32448	circumsporozoite p
39	48	37.8	778	2	A64656	hypothetical prote
40	48	37.8	778	2	C71944	hypothetical prote
41	48	37.8	1714	2	E71609	Ser/Thr protein k1
42	47.5	37.4	264	2	F85927	hypothetical prote
43	47.5	37.4	264	2	H65058	hypothetical prote
44	47.5	37.4	598	2	C81281	glutamine-fructos
45	47	37.0	175	2	G71480	hypothetical prote

## ALIGNMENTS

RESULT 1  
OZQOAF  
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate INTW22)  
C:Species: Plasmodium falciparum  
C:Date: 15-Nov-1984 #sequence\_revision 15-Nov-1984 #text\_change 09-Jun-2000  
C:Accession: A03388  
R:Idame, J.B.; Williams, J.L.; McCutchan, T.F.; Weber, J.L.; Wiltz, R.A.; Hochmeyer, W  
Science 225, 593-599, 1984  
A:Title: Structure of the gene encoding the immunodominant surface antigen on the spo  
A:Reference number: A03388; MUID:84250215  
A:Accession: A03388  
A:Molecule type: DNA  
A:Residues: 1-412 <DAM>  
A:Cross-References: GB:K02194; NID:9160160; PIDN:AAA29524.1; PID:9160161  
A:Experimental source: clone 7G8  
C:Comment: Residues 1-16 are the probable signal sequence.  
C:Comment: There are 41 copies of a 4-residue repeating unit in the middle domain of  
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology  
F:336-390/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 100.0%; Score 127; DB 1; Length 412;  
Best Local Similarity 100.0%; Pred. No. 8e-10;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPKDELVDYENDIEKKICKMEKCS 23  
|||||  
Db 368 KPKDELVDYENDIEKKICKMEKCS 390

RESULT 2  
A54533  
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain T4, Thai  
C:Species: Plasmodium falciparum  
C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jun-2000  
C:Accession: A54533  
R:del Portillo, H.A.; Nussenzweig, R.S.; Enea, V.  
Mol. Biochem. Parasitol. 24, 289-294, 1987  
A:Title: Circumsporozoite gene of a Plasmodium falciparum strain from Thailand.  
A:Reference number: A54533; MUID:87315205  
A:Accession: A54533  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-424 <DEL>  
A:Cross-References: GB:M19752; NID:9160216; PIDN:AAA29555.1; PID:9160217  
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology  
F:348-402/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 100.0%; Score 127; DB 2; Length 424;  
Best Local Similarity 100.0%; Pred. No. 8.2e-10;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPKDELVDYNDIEKKICKMEKCS 23  
|||||  
DB 380 KPKDELVDYNDIEKKICKMEKCS 402

RESULT 3  
A54529  
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain Wellcome)

C:Species: Plasmodium falciparum  
C>Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jun-2000  
C:Accession: A54529  
R:Lockyer, M.J.; Schwarz, R.T.  
Mol. Biochem. Parasitol. 22, 101-108, 1987  
A:Title: Strain variation in the circumsporozoite protein gene of Plasmodium falciparum.  
A:Reference number: A54529; MUID:87115616  
A:Accession: A54529  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-442 <LOC>  
A:Cross-references: GB:M15505; NID:g160214; PIDN:AAA29554.1; PID:g160215  
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology  
C:Keywords: tandem repeat  
F:366-420/Domain: thrombospondin type 1 repeat homology <THRI>

Query Match 97.6%; Score 124; DB 2; Length 442;  
Best Local Similarity 95.7%; Pred. No. 2.2e-09;  
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPKDELVDYNDIEKKICKMEKCS 23  
|||||  
DB 398 KPKDELVDYNDIEKKICKMEKCS 420

RESULT 4  
A39756  
circumsporozoite protein - Plasmodium reichenowi

C:Species: Plasmodium reichenowi  
C>Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 20-Aug-1999  
C:Accession: A39756  
R:Lal, A.A.; Goldman, I.F.  
J. Biol. Chem. 266, 6686-6689, 1991  
A:Title: Circumsporozoite protein gene from Plasmodium reichenowi, a chimpanzee malaria  
A:Reference number: A39756; MUID:91201303  
A:Accession: A39756  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-588 <LOC>  
A:Cross-references: GB:M60972; NID:g160228; PIDN:AAA29561.1; PID:g160229  
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology  
F:312-366/Domain: thrombospondin type 1 repeat homology <THRI>

Query Match 96.1%; Score 122; DB 2; Length 388;  
Best Local Similarity 91.3%; Pred. No. 3.6e-09;  
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPKDELVDYNDIEKKICKMEKCS 23  
|||||  
DB 344 KPKDELVDYNDIEKKICKMEKCS 366

RESULT 5  
S05428  
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate NF54)

C:Species: Plasmodium falciparum  
C>Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 09-Jun-2000  
C:Accession: S05428; A45527; I60657  
R:Campbell, J.R.  
Nucleic Acids Res. 17, 5854, 1989  
A:Title: DNA sequence of the gene encoding a Plasmodium falciparum malaria candidate vac  
A:Reference number: S05428; MUID:89345189

A:Accession: S05428

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-405 <CAM>

A:Cross-references: EMBL:X15363

R:Caspers, P.; Gentz, R.; Matile, H.; Pink, J.R.; Sinigaglia, F.

Mol. Biochem. Parasitol. 35, 185-190, 1989

A:Title: The circumsporozoite protein gene from NF54, a Plasmodium falciparum isolate

A:Reference number: A45527; MUID:89364998

A:Accession: A45527

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-405 <CAS>

A:Cross-references: GB:M22982; GB:J04650; NID:g160168; PIDN:AAA29527.1; PID:g160169

R:Lockyer, M.J.; Marsh, K.; Newbold, C.I.

Mol. Biochem. Parasitol. 37, 275-280, 1989

A:Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell

A:Reference number: A60657; MUID:90114334

A:Accession: A60657

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 319-336,354-373 <LOC>

A:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology

F:329-383/Domain: thrombospondin type 1 repeat homology <THRI>

Query Match 95.3%; Score 121; DB 2; Length 405;  
Best Local Similarity 95.7%; Pred. No. 5.2e-09;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPKDELVDYNDIEKKICKMEKCS 23  
|||||  
DB 361 KPKDELVDYNDIEKKICKMEKCS 383

RESULT 6  
C60657  
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate 7G8) (fr

C:Species: Plasmodium falciparum

C>Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 09-Jun-2000

C:Accession: C60657

R:Lockyer, M.J.; Marsh, K.; Newbold, C.I.

Mol. Biochem. Parasitol. 37, 275-280, 1989

A:Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell

A:Reference number: A60657; MUID:90114334

A:Accession: C60657

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-38 <LOC>

C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology

Query Match 55.9%; Score 71; DB 2; Length 38;  
Best Local Similarity 100.0%; Pred. No. 0.0035;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPKDELVDYNDIE 13  
|||||  
DB 26 KPKDELVDYNDIE 38

RESULT 7  
D60657  
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate Wel) (fr

C:Species: Plasmodium falciparum

C>Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 09-Jun-2000

C:Accession: D60657

R:Lockyer, M.J.; Marsh, K.; Newbold, C.I.

Mol. Biochem. Parasitol. 37, 275-280, 1989

A:Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell

A:Reference number: A60657; MUID:90114334

A:Accession: D60657

A:Status: preliminary; not compared with conceptual translation



A:Molecule type: DNA  
A:Residues: 1-38 <LOC>  
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology

Query Match 53.5%; Score 68; DB 2; Length 38;  
Best Local Similarity 92.3%; Pred. No. 0.009;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPKDELDYENDIE 13  
||||:|||||||  
DB 26 KPKDQLDYANDIE 38

RESULT 8  
E60657  
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate Itc2) (frag  
C:Species: Plasmodium falciparum  
C:Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 09-Jun-2000  
C:Accession: E60657  
R:Lockyer, M.J.; Marsh, K.; Newbold, C.I.  
Mol. Biochem. Parasitol. 37, 275-280, 1989  
A:Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell ef  
A:Reference number: A60657; MUID:90114334  
A:Accession: E60657  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-38 <LOC>  
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology

Query Match 53.5%; Score 68; DB 2; Length 38;  
Best Local Similarity 92.3%; Pred. No. 0.009;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPKDELDYENDIE 13  
||||:|||||||  
DB 26 KPKDQLDYANDIE 38

RESULT 9  
A38869  
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate 427-5) (fra  
C:Species: Plasmodium falciparum  
C:Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 09-Jun-2000  
C:Accession: A38869  
R:Lockyer, M.J.; Marsh, K.; Newbold, C.I.  
Mol. Biochem. Parasitol. 37, 275-280, 1989  
A:Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell ef  
A:Reference number: A60657; MUID:90114334  
A:Accession: A38869  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-38 <LOC>  
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology

Query Match 51.2%; Score 65; DB 2; Length 38;  
Best Local Similarity 92.3%; Pred. No. 0.023;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPKDELDYENDIE 13  
|||||||  
DB 26 KPKDELDYANDIE 38

RESULT 10  
B60657  
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate T9-98) (fra  
C:Species: Plasmodium falciparum  
C:Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 09-Jun-2000  
C:Accession: B60657  
R:Lockyer, M.J.; Marsh, K.; Newbold, C.I.

Mol. Biochem. Parasitol. 37, 275-280, 1989  
A:Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell  
A:Reference number: A60657; MUID:90114334  
A:Accession: B60657  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-38 <LOC>  
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology

Query Match 51.2%; Score 65; DB 2; Length 38;  
Best Local Similarity 92.3%; Pred. No. 0.023;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPKDELDYENDIE 13  
|||||||  
DB 26 KPKDQLDYANDIE 38

RESULT 11  
H60657  
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate 406-10)  
C:Species: Plasmodium falciparum  
C:Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 09-Jun-2000  
C:Accession: H60657  
R:Lockyer, M.J.; Marsh, K.; Newbold, C.I.  
Mol. Biochem. Parasitol. 37, 275-280, 1989  
A:Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell  
A:Reference number: A60657; MUID:90114334  
A:Accession: H60657  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-38 <LOC>  
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology

Query Match 49.6%; Score 63; DB 2; Length 38;  
Best Local Similarity 84.6%; Pred. No. 0.043;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPKDELDYENDIE 13  
||||:|||||||  
DB 26 KPKDQLDYANDIE 38

RESULT 12  
B38869  
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate 366-2) (f  
C:Species: Plasmodium falciparum  
C:Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 09-Jun-2000  
C:Accession: B38869  
R:Lockyer, M.J.; Marsh, K.; Newbold, C.I.  
Mol. Biochem. Parasitol. 37, 275-280, 1989  
A:Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell  
A:Reference number: A60657; MUID:90114334  
A:Accession: B38869  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-38 <LOC>  
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology

Query Match 49.6%; Score 63; DB 2; Length 38;  
Best Local Similarity 84.6%; Pred. No. 0.043;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPKDELDYENDIE 13  
||||:|||||||  
DB 26 KPKDQLDYANDIE 38

RESULT 13  
G60657

circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate 366-8) (fr  
 C:Species: Plasmodium falciparum  
 C:Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 09-Jun-2000  
 C:Accession: G60657  
 R:Lockyer, M.J.; Marsh, K.; Newbold, C.I.  
 Mol. Biochem. Parasitol. 37, 275-280, 1989  
 A:Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell ep  
 A:Reference number: A60657; MUID:90114334  
 A:Accession: G60657  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-38 <LOC>  
 C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology

Query Match 48.8%; Score 62; DB 2; Length 38;  
 Best Local Similarity 84.6%; Pred. No. 0.059; 1; Mismatches 0; Gaps 0;  
 Matches 11; Conservative 1; Indels 0; Gaps 0;  
 QY 1 KPKDELVDYNDIE 13  
 ||||:||||  
 DB 26 KPKDQLDYNDIE 38

RESULT 14  
 F60657  
 circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate 366-1) (fr  
 C:Species: Plasmodium falciparum  
 C:Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 09-Jun-2000  
 C:Accession: F60657  
 R:Lockyer, M.J.; Marsh, K.; Newbold, C.I.  
 Mol. Biochem. Parasitol. 37, 275-280, 1989  
 A:Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell ep  
 A:Reference number: A60657; MUID:90114334  
 A:Accession: F60657  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-38 <LOC>  
 C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology

Query Match 48.8%; Score 62; DB 2; Length 38;  
 Best Local Similarity 84.6%; Pred. No. 0.059; 1; Mismatches 0; Gaps 0;  
 Matches 11; Conservative 1; Indels 0; Gaps 0;  
 QY 1 KPKDELVDYNDIE 13  
 ||||:||||  
 DB 26 KPKDQLDYNDIE 38

RESULT 15  
 B29795  
 circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain LB5) (fragme  
 C:Species: Plasmodium falciparum  
 C:Date: 18-Oct-1989 #sequence\_revision 21-Jul-1995 #text\_change 09-Jun-2000  
 C:Accession: B29795; A60657  
 R:de la Cruz, V.F.; Lal, A.A.; McCutchan, T.F.  
 J. Biol. Chem. 262, 11935-11939, 1987  
 A:Title: Sequence variation in putative functional domains of the circumsporozoite prote  
 A:Reference number: A92609; MUID:87308186  
 A:Accession: B29795  
 A:Molecule type: DNA  
 A:Residues: 1-161 <DEL>  
 A:Cross-references: GB:M17802; GB:M17803; GB:M17806  
 R:Lockyer, M.J.; Marsh, K.; Newbold, C.I.  
 Mol. Biochem. Parasitol. 37, 275-280, 1989  
 A:Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell ep  
 A:Reference number: A60657; MUID:90114334  
 A:Accession: A60657  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 152-189 <LOC>  
 C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology

Query Match 48.8%; Score 62; DB 2; Length 189;  
 Best Local Similarity 84.6%; Pred. No. 0.26; 1; Mismatches 0; Gaps 0;  
 Matches 11; Conservative 1; Indels 0; Gaps 0;  
 QY 1 KPKDELVDYNDIE 13  
 ||||:||||  
 DB 177 KPKDQLDYNDIE 189

Search completed: January 29, 2002, 10:26:36  
 Job time: 647 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 11:13:38 ; Search time 80.65 Seconds  
(without alignments)  
10.456 Million cell updates/sec

Title: US-09-763-397A-6  
Perfect score: 127  
Sequence: 1 KPDELDYNDIEKKICKMEKCS 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	127	100.0	412	1	CSP_PLAFA
2	127	100.0	424	1	CSP_PLAFT
3	124	97.6	442	1	CSP_PLAFW
4	122	96.1	388	1	CSP_PLARE
5	121	95.3	397	1	CSP_PLARO
6	60.5	47.6	378	1	CSP_PLACB
7	60.5	47.6	378	1	CSP_PLACL
8	60.5	47.6	398	1	CSP_PLACC
9	60.5	47.6	401	1	CSP_PLACG
10	60.5	47.6	419	1	CSP_PLACM
11	58.5	46.1	339	1	CSP_PLABE
12	58.5	46.1	347	1	CSP_PLABA
13	56.5	44.5	367	1	CSP_PLATO
14	53	41.7	177	1	SHAO_YEAST
15	51	40.2	343	1	CSP_PLAVS
16	51	40.2	378	1	CSP_PLAVB
17	51	40.2	386	1	CSP_PLAST
18	49	38.6	393	1	CSP_PLABR
19	49	38.6	429	1	CSP_PLAKA
20	48	37.8	629	1	DNK_STRAP
21	47	37.0	613	1	DNK_IACSK
22	47	37.0	720	1	NUP2_YEAST
23	46.5	36.6	663	1	UVRA_AQUAE
24	46	36.2	253	1	Y990_CAME
25	45.5	35.8	321	1	MCH_METBA
26	45	35.4	388	1	CZFI_CANAL
27	45	35.4	492	1	SYRM_YEAST
28	45	35.4	590	1	DNK_STRMU
29	45	35.4	607	1	DNK_STRAG
30	45	35.4	609	1	DNK_STRYG
31	45	35.4	721	1	PRTP_HSV7J
32	44.5	35.0	315	1	MCH_METKA
33	44	34.6	345	1	ALF2_ALCEU

34	44	34.6	607	1	DNK_STRPN	P95829 streptococ
35	44	34.6	931	1	CC21_SCHPO	P29458 schizosacch
36	44	34.6	1018	1	HTRA_CHICK	P79987 gallus gall
37	44	34.6	1070	1	YHV4_YEAST	P38850 saccharomyc
38	44	34.6	3866	1	HRX_MOUSE	P55200 mus musculu
39	44	34.6	3969	1	HRX_HUMAN	P03164 homo sapien
40	43.5	34.3	514	1	SYS_METMY	O30520 mechanococ
41	43.5	34.3	630	1	Y242_MYCE	P47484 mycoplasma
42	43.5	34.3	1272	1	UBP2_YEAST	O01476 saccharomyc
43	43.5	34.3	5179	1	MUC2_HUMAN	O02817 homo sapien
44	43	33.9	365	1	GLN2_DROME	P20478 drosophila
45	43	33.9	372	1	RECA_STRAM	P41054 streptomyce

## ALIGNMENTS

RESULT 1	ID	CSP_PLAFA	STANDARD:	PRT:	412 AA.
AC	P02893:				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	20-AUG-2001 (Rel. 40, Last annotation update)				
DE	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).				
OS	Plasmodium falciparum.				
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.				
OX	NCBI_TaxID=5613;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=84250215; PubMed=6204383;				
RA	Dane J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,				
RA	Hochmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,				
RA	Sanders G.S., Reddy B.P., Diggs C.L., Miller L.H.;				
RT	"Structure of the gene encoding the immunodominant surface antigen on				
RT	the sporozoite of the human malaria parasite Plasmodium falciparum.";				
RL	Science 225:593-599(1984).				
CC	-I- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT				
CC	SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE				
CC	MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE				
CC	VERTEBRATE HOST).				
CC	-I- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR				
CC	ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES				
CC	WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.				
CC	-I- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.				
CC					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	entities requires a license agreement (See <a href="http://www.isb-sdb.ch/announce/">http://www.isb-sdb.ch/announce/</a>				
CC	or send an email to <a href="mailto:license@sdb.ch">license@sdb.ch</a> ).				
CC					
DR	EMBL: K02194; AAA29524.1; -				
DR	PIR: A03388; OZQAF.				
DR	InterPro: IPR003067; Circmsprzoite.				
DR	InterPro: IPR000884; TSP1.				
DR	Pfam: PF00090; TSP_1; 1.				
DR	PRINTS: PR01303; CRCMSPRZOITE.				
DR	SMART: SM00209; TSP1; 1.				
KW	Malaria; Sporozoite; Repeat; Signal.				
FT	SIGNAL 1				
FT	CHAIN 17 412				
FT	DOMAIN 123 290				
SO	SEQUENCE 412 AA; 44420 MW; 1EEED3DE0965F8 CRC64;				
QY	1 KPDELDYNDIEKKICKMEKCS 23				

Query Match 100.0% Score 127; DB 1; Length 412;

Best Local Similarity 100.0% Pred. No. 5.9e-10; Mismatches 0; Indels 0; Gaps 0;

Db 368 KPDLDYENDIEKKICKMEKCS 390

```

RESULT 2
CSP_PLAFW STANDARD: PRT: 424 AA.
ID CSP_PLAFW
AC P13814:
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-AUG-1998 (Rel. 08, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
OS Plasmodium falciparum (isolate t4 / Thailand).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5846;

[1]
SEQUENCE FROM N.A.
MEDLINE=8715205; Pubmed=3306373;
RA del Portillo H.A., Nussenzweig R.S., Enea V.;
RT "Circumsporozoite gene of a Plasmodium falciparum strain from Thailand."
RL Mol. Biochem. Parasitol. 24:289-294(1987).
CC -1- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE VERTEBRATE HOST).
CC -1- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
CC -1- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC
CC EMBL: M19752; AAA29555.1; -.
CC PIR: A54533; A54533.
CC InterPro: IPR003067; Crcmsprzoite.
CC Pfam: PF00090; tsp_1; 1.
CC PRINTS: PR01303; Crcmsprzoite.
CC SMART: SMO0209; TSP1; 1.
KM Malaria; Sporozoite; Repeat; Signal.
FT SIGNAL 1 16 CIRCUMSPOROZOITE PROTEIN.
FT CHAIN 17 424 45 X 4 AA TANDM REPEATS OF N-A-N-P.
FT DOMAIN 123 300
SO SEQUENCE 424 AA; 45610 MW; 710AB14238786CD9 CRC64;

Query Match 100.0%; Score 127; DB 1; Length 424;
Best Local Similarity 100.0%; Pred. No. 6; 1e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPDLDYENDIEKKICKMEKCS 23
Db 380 KPDLDYENDIEKKICKMEKCS 402

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87115616; Pubmed=3543671;
RA Lockyer M.J., Schwarz R.T.;
RT "Strain variation in the circumsporozoite protein gene of Plasmodium falciparum."
RL Mol. Biochem. Parasitol. 22:101-108(1987).
CC -1- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE VERTEBRATE HOST).
CC -1- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
CC -1- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
CC
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CC
CC EMBL: M15505; AAA29554.1; -.
CC PIR: A54529; A54529.
CC InterPro: IPR003067; Crcmsprzoite.
CC Pfam: PF00090; tsp_1; 1.
CC PRINTS: PR01303; Crcmsprzoite.
CC SMART: SMO0209; TSP1; 1.
KM Malaria; Sporozoite; Repeat; Signal.
FT SIGNAL 1 16 CIRCUMSPOROZOITE PROTEIN.
FT CHAIN 17 442 47 X 4 AA TANDM REPEATS OF N-A-N-P.
FT DOMAIN 130 320
SO SEQUENCE 442 AA; 47402 MW; BD57A9A152B85E03 CRC64;

Query Match 97.6%; Score 124; DB 1; Length 442;
Best Local Similarity 95.7%; Pred. No. 1; 6e-09;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPDLDYENDIEKKICKMEKCS 23
Db 398 KPDLDYENDIEKKICKMEKCS 420

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-1- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.  
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CC -----  
DR EMBL: M60972; AAA29561.1; -  
DR PIR: A39756; A39756.  
DR InterPro: IPR003067; Circmsporzoite.  
DR Pfam: PF00090; tsp.1; 1.  
DR PRINTS: PR01303; Circmsporzoite.  
DR SMART: SM00209; TSP1.1  
KW Malaria; Sporozoite; Repeat; Signal.  
FT SIGNAL 1 16 PROBABLE.  
FT CHAIN 17 388 CIRCUMSPOROZOITE PROTEIN.  
FT DOMAIN 120 267 62 X 4 AA TANDEM REPEATS OF N-A-N-P.  
SQ SEQUENCE 388 AA; 42245 MW; C031EEFBE2E35604 CRC64;

Query Match 96.1%; Score 122; DB 1; Length 388;  
Best Local Similarity 91.3%; Pred. No. 2.6e-09;  
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPKDELVDYNDIEKKICKMEKCS 23  
|||:||||:||||:||||:||||:  
Db 344 KPKDLDYNDIEKKICKMEKCS 366

RESULT 5  
CSP\_PLAFO STANDARD; PRT: 397 AA.  
ID CSP\_PLAFO  
AC P19597; Q25798;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).  
OS Plasmodium falciparum (isolate NF54).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5843;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89345189; PubMed=2668895;  
RA Campbell J.R.;  
RT "DNA sequence of the gene encoding a Plasmodium falciparum malaria  
RT candidate vaccine antigen";  
RL Nucleic Acids Res. 17:5854-5854(1989).  
RN [2]  
RP REVISIONS.  
RA Campbell J.R.;  
RL Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92155298; PubMed=1346766;  
RA Davys J.R., Cortese J.F., Herington D.A., Murphy J.R., Clyde D.F.,  
RA Thomas A.W., Bagar S., Cochran M.A., Thanassi J., Levine M.M.,  
RA Hackett C.S.;  
RT "Plasmodium falciparum: in vitro characterization and human  
RT infectivity of a cloned line";  
RL Exp. Parasitol. 74:159-168(1992).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89364998; PubMed=2671723;  
RA Caspers P., Gentz R., Matile H., Pink J.R., Slingagla F.;  
RT "The circumsporozoite protein gene from NF54, a Plasmodium falciparum  
RT isolate used in malaria vaccine trials";  
RL Mol. Biochem. Parasitol. 35:185-190(1989).  
CC -1- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT  
CC SURFACE ANTIGEN ON THE SPOOROZOITE (THE INFECTIVE STAGE OF THE

CC MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE  
CC VERTEBRATE HOST).  
CC -1- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR  
CC ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES  
CC WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.  
CC -1- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.  
CC -----  
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CC -----  
DR EMBL: X15363; CAA33421.1; -  
DR EMBL: M83886; AAA29521.1; -  
DR EMBL: M22982; AAA29527.1; -  
DR PIR: S05428; S05428.  
DR PIR: A45527; A45527.  
DR InterPro: IPR003067; Circmsporzoite.  
DR SMART: SM00209; TSP1.1  
DR Pfam: PF00090; tsp.1; 1.  
DR PRINTS: PR01303; Circmsporzoite.  
DR SMART: SM00209; TSP1.1  
KW Malaria; Sporozoite; Repeat; Signal.  
FT SIGNAL 1 16 PROBABLE.  
FT CHAIN 17 397 CIRCUMSPOROZOITE PROTEIN.  
FT DOMAIN 101 272 43 X 4 AA TANDEM REPEATS OF N-A-N-P.  
FT CONFLICT 194 194 A -> ANPANPNA (IN REF. 4).  
SQ SEQUENCE 397 AA; 42646 MW; 9E81146F59BCEA3 CRC64;

Query Match 95.3%; Score 121; DB 1; Length 397;  
Best Local Similarity 95.7%; Pred. No. 3.6e-09;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPKDELVDYNDIEKKICKMEKCS 23  
|||||:|||||:|||||:|||||:  
Db 353 KPKDELVDYNDIEKKICKMEKCS 375

RESULT 6  
CSP\_PLACB STANDARD; PRT: 378 AA.  
ID CSP\_PLACB  
AC P08672;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).  
OS Plasmodium cynomolgi (strain Berok).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5828;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87102878; PubMed=3802196;  
RA Galinski M.R., Arnot D.E., Cochran A.H., Barnwell J.W.,  
RA Nussenzweig R.S., Enea V.;  
RT "The circumsporozoite gene of the Plasmodium cynomolgi complex";  
RL Cell 48:311-319(1987).  
CC -1- DOMAIN: THERE ARE 10 TANDEM COPIES OF A 9-RESIDUE REPEAT (PRECEDED  
CC BY A 6-RESIDUE INCOMPLETE REPEAT) AND 3 TANDEM COPIES OF A 16-  
CC RESIDUE REPEAT (FOLLOWED BY 3 SHORTER, INCOMPLETE COPIES).  
CC -1- MISCELLANEOUS: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT  
CC SURFACE ANTIGEN ON THE SPOOROZOITE (THE INFECTIVE STAGE OF THE  
CC MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE  
CC VERTEBRATE HOST).  
CC -1- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR  
CC ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES  
CC WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.  
CC -1- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.  
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DR EMBL: M15104; AAA29532.1; -  
 DR PIR: D26255; OZQ0AB.  
 DR InterPro: IPR003067; Crcmsprzoite.  
 DR InterPro: IPR000884; TSP1.

DR Pfam: PF00090; TSP1; 1.  
 DR PRINTS: PR01303; Crcmsprzoite.

DR SMART: SM00209; TSP1; 1.

KW Malaria; Sporozoite; Repeat; Signal.  
 FT SIGNAL 1 19 PROBABLE.  
 FT CHAIN 20 378 CIRCUMSPOROZOITE PROTEIN.  
 FT DOMAIN 97 192 10.5 X 9 AA REPEATS.

FT DOMAIN 193 240 3 X 16 AA TANDEM REPEATS.  
 FT REPEAT 241 251  
 FT REPEAT 252 260  
 FT REPEAT 261 268

SEQUENCE 378 AA: 36286 MW: 779BA081C140793F CRC64;

Query Match 47.6%; Score 60.5; DB 1; Length 378;  
 Best Local Similarity 47.8%; Pred. No. 0.43;  
 Matches 11; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

OY 1 KPELDYENDIEKKICKMEKCS 23  
 I :||| ||:|:| ||:|:

DB 335 KPELDV-NDLETVCTMDKCA 356.

RESULT 7  
 CSP\_PLACC STANDARD; PRT: 378 AA.  
 ID CSP\_PLACC  
 AC P08673;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).  
 OS Plasmodium cynomolgi (strain London).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 ON NCBI\_TaxId=5831;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87102878; PubMed=3802196;  
 RA Galinski M.R., Arnot D.E., Cochrane A.H., Barnwell J.W.,  
 RA Nussenzweig R.S., Enea V.;  
 RT "The circumsporozoite gene of the Plasmodium cynomolgi complex.";  
 RL Cell 48:311-319(1987).

CC -1- MISCELLANEOUS: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT  
 CC SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE  
 CC MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE  
 CC VERTEBRATE HOST).  
 CC -1- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR  
 CC ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES  
 CC WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.

CC -1- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.  
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DR EMBL: M15104; AAA29537.1; -  
 DR PIR: A26255; OZQ0AL.  
 DR InterPro: IPR003067; Crcmsprzoite.  
 DR InterPro: IPR000884; TSP1.

DR Pfam: PF00090; TSP1; 1.  
 DR PRINTS: PR01303; Crcmsprzoite.  
 DR SMART: SM00209; TSP1; 1.

KW Malaria; Sporozoite; Repeat; Signal.  
 FT SIGNAL 1 19 PROBABLE.  
 FT CHAIN 20 378 CIRCUMSPOROZOITE PROTEIN.  
 FT DOMAIN 98 211 18 X 6 AA TANDEM REPEATS OF D-G-A-R-A-  
 FT [EA].

FT DOMAIN 212 277 6 X 11 AA TANDEM REPEATS OF G-N-O-A-G-G-  
 FT O-A-G-A-G.  
 FT SEQUENCE 378 AA: 37462 MW: 8295A913C36420C5 CRC64;

Query Match 47.6%; Score 60.5; DB 1; Length 378;  
 Best Local Similarity 47.8%; Pred. No. 0.43;  
 Matches 11; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

OY 1 KPELDYENDIEKKICKMEKCS 23  
 I :||| ||:|:| ||:|:

DB 335 KPELDV-NDLETVCTMDKCA 356

RESULT 8  
 CSP\_PLACC STANDARD; PRT: 398 AA.  
 ID CSP\_PLACC  
 AC P08673;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).  
 OS Plasmodium cynomolgi (strain Ceylon).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 ON NCBI\_TaxId=5829;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87102878; PubMed=3802196;  
 RA Galinski M.R., Arnot D.E., Cochrane A.H., Barnwell J.W.,  
 RA Nussenzweig R.S., Enea V.;  
 RT "The circumsporozoite gene of the Plasmodium cynomolgi complex.";  
 RL Cell 48:311-319(1987).

CC -1- MISCELLANEOUS: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT  
 CC SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE  
 CC MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE  
 CC VERTEBRATE HOST).  
 CC -1- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR  
 CC ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES  
 CC WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.

CC -1- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.  
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DR EMBL: M15103; AAA29533.1; -  
 DR PIR: C26255; OZQ0AS.  
 DR InterPro: IPR003067; Crcmsprzoite.  
 DR InterPro: IPR000884; TSP1.  
 DR Pfam: PF00090; TSP1; 1.  
 DR PRINTS: PR01303; Crcmsprzoite.  
 DR SMART: SM00209; TSP1; 1.  
 KW Malaria; Sporozoite; Repeat; Signal.  
 FT SIGNAL 1 19 PROBABLE.  
 FT CHAIN 20 398 CIRCUMSPOROZOITE PROTEIN.  
 FT DOMAIN 97 249 17 X 9 AA TANDEM REPEATS OF A-G-N-N-A-A-  
 FT A-G-E.

SEQUENCE 398 AA: 37718 MW: 6DFA2E8A62ED055F CRC64;

Query Match 47.6%; Score 60.5; DB 1; Length 398;



Best Local Similarity 47.8%, Pred. No. 0.45;  
Matches 11: Conservative 6; Mismatches 5; Indels 1; Gaps 1;  
OY 1 KPKDELVDYNDIEKKICKMEKCS 23  
DB 355 KKPELDV-ANDETEVCTMDKCA 376

RESULT 9  
CSP\_PLACG STANDARD: PRT: 401 AA.  
AC P06874;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).  
OS Plasmodium cynomolgi (strain Gomdak).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5830;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=87102878; PubMed=3802196;  
RA Galinski M.R., Arnot D.E., Cochran A.H., Barnwell J.W.,  
RA Nussenzweig R.S., Enea V.;  
RT "The circumsporozoite gene of the Plasmodium cynomolgi complex.";  
RL Cell 48:311-319(1987).  
CC -1- MISCELLANEOUS: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT  
CC SURFACE ANTIGEN ON THE SPOOROZOITE (THE INFECTIVE STAGE OF THE  
CC MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE  
CC VERTEBRATE HOST).  
CC -1- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR  
CC ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES  
CC WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.  
CC -1- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.  
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DR EMBL: M15100; AAA29536.1; -  
DR PIR: E26255; OZQAC.  
DR InterPro: IPR003067; Circmsprzoite.  
DR InterPro: IPR000884; TSP1.  
DR Pfam: PF00090; tsp\_1; 1.  
DR PRINTS: PR01303; CRCMSPRZOITE.  
DR SMART: SM00209; TSP1; 1.  
DR Malaria; Sporozoite; Repeat; Signal.  
FT SIGNAL 1 19 PROBABLE.  
FT CHAIN 20 401 CIRCUMSPOROZOITE PROTEIN.  
FT DOMAIN 98 278 17 X 11 AA TANDEM REPEATS OF [DG]-G-A-A-  
FT A-A-G-G-G-N.  
SO SEQUENCE 401 AA; 36664 MW; 57D666268238503E CRC64;

Query Match 47.6%, Score 60.5; DB 1; Length 401;  
Best Local Similarity 47.8%; Pred. No. 0.45;  
Matches 11: Conservative 6; Mismatches 5; Indels 1; Gaps 1;

OY 1 KPKDELVDYNDIEKKICKMEKCS 23  
DB 358 KKPELDV-ANDETEVCTMDKCA 379

RESULT 10  
CSP\_PLACM STANDARD: PRT: 419 AA.  
AC P06876;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).  
OS Plasmodium cynomolgi (strain Mulligan/NH).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5832;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=87102878; PubMed=3802196;  
RA Galinski M.R., Arnot D.E., Cochran A.H., Barnwell J.W.,  
RA Nussenzweig R.S., Enea V.;  
RT "The circumsporozoite gene of the Plasmodium cynomolgi complex.";  
RL Cell 48:311-319(1987).  
CC -1- MISCELLANEOUS: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT  
CC SURFACE ANTIGEN ON THE SPOOROZOITE (THE INFECTIVE STAGE OF THE  
CC MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE  
CC VERTEBRATE HOST).  
CC -1- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR  
CC ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES  
CC WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.  
CC -1- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.  
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DR EMBL: M15102; AAA29539.1; -  
DR PIR: B26255; OZQAM.  
DR InterPro: IPR003067; Circmsprzoite.  
DR InterPro: IPR000884; TSP1.  
DR Pfam: PF00090; tsp\_1; 1.  
DR PRINTS: PR01303; CRCMSPRZOITE.  
DR SMART: SM00209; TSP1; 1.  
DR Malaria; Sporozoite; Repeat; Signal.  
FT SIGNAL 1 19 PROBABLE.  
FT CHAIN 20 419 CIRCUMSPOROZOITE PROTEIN.  
FT DOMAIN 99 314 54 X 4 AA TANDEM REPEATS OF N-A-[DG]-G.  
SO SEQUENCE 419 AA; 38924 MW; 8F46CDB8A1B4E5F4 CRC64;

Query Match 47.6%, Score 60.5; DB 1; Length 419;  
Best Local Similarity 47.8%; Pred. No. 0.47;  
Matches 11: Conservative 6; Mismatches 5; Indels 1; Gaps 1;

OY 1 KPKDELVDYNDIEKKICKMEKCS 23  
DB 376 KKPELDV-NDLETEVCTMDKCA 397

RESULT 11  
CSP\_PLABE STANDARD: PRT: 339 AA.  
AC P06915;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).  
OS Plasmodium berghei.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5821;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=87089740; PubMed=2423395;  
RA Eichinger D.J., Arnot D.E., Tam J.P., Nussenzweig V., Enea V.;  
RT "Circumsporozoite protein of Plasmodium berghei: gene cloning and  
RT identification of the immunodominant epitopes.";  
RL Mol. Cell. Biol. 6:3965-3972(1986).  
CC -1- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT  
CC SURFACE ANTIGEN ON THE SPOOROZOITE (THE INFECTIVE STAGE OF THE  
CC MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE

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CC VERBERGATE HOST).  
CC MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR  
CC ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES  
CC WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.  
CC -1- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.  
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CC DR EMBL; M1A135; AAA29577.1; .  
CC DR PIR; A25083; OZQOM. Crmsprzoite.  
CC DR InterPro; IPR003067; Crmsprzoite.  
DR InterPro; IPR000884; TSP1.  
CC Pfam; PF00090; tsp_1; 1.  
DR PRINTS; PR01303; CRMSPRZOITE.  
DR SMART; SMO0209; TSP1; 1.  
CC PROSITE; PS50092; TSP1; 1.  
KW Malaria; Sporozoite; Repeat; Signal.  
FT SIGNAL 1 23 PROBABLE.  
FT CHAIN 24 339 CIRCUMSPOROZOITE PROTEIN.  
FT DOMAIN 93 196 13 X 8 AA TANDEM REPEATS.  
FT DOMAIN 206 238 16 X 2 AA TANDEM REPEATS OF P-Q.  
FT FT FT  
SQ SEQUENCE 339 AA; 37138 MW; E806B46D1D9551B CRC64;  
  
QY Query Match 46.1%; Score 58.5; DB 1; Length 339;  
Best Local Similarity 52.2%; Pred. No. 0.71;  
Matches 12; Conservative 5; Mismatches 5; Indels 1; Gaps 1;  
  
Db 1 KPNDELVDENDIEKKICKMKCS 23  
296 KRAEDLTLE-DIDTEICKMDKCS 317  
  
RESULT 12  
CSP_PLABA STANDARD; PRT; 347 AA.  
ID CSP_PLABA  
AC P23093;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).  
OS Plasmodium berghei (strain Anka) .  
OC Eukaryota; Alveolata; Apicomplexa; Hemosporida; Plasmodium.  
OX NCBI_TaxID=5823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90221834; PubMed=2183186;  
RA Lockyer M.J., Davies C.S., Subdier A., Sindén R.E.;  
CC "Nucleotide sequence of the Plasmodium berghei circumsporozone  
protein gene from the ANKA clone 2.34f." ;  
RL Nucleic Acids Res. 18:376-376(1990) .  
RT RT  
RT FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT  
CC -I- SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE  
CC MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE  
CC VERBERGATE HOST).  
CC -I- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR  
CC ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES  
CC WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.  
CC -I- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.  
-----  
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DR EMBL: X17606; CAA35608.1; -
DR PIR: S07873; OZ20BK.
DR InterPro: IPR003067; Crcmsporzoite.
DR InterPro: IPR000884; TSP1.
DR Pfam: PF00090; tsp.1; 1.
DR PRINTS: PR01303; CRCMSPORZOITE.
DR SMART: SM00209; TSP1. 1.
DR PROSITE: PS0092; TSP1. 1.
DR Malaria; Sporozoite; Repeat; Signal.
KM SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 347 CIRCUMSPOROZOITE PROTEIN.
FT DOMAIN 93 204 13 X 8 AA REPEATS.
FT DOMAIN 214 247 17 X 2 AA REPEATS OF P-Q.
FT SEQUENCE 347 AA; 37776 MW; 0EC240EE35681AF8 CRC64;

Query Match 46.1%; Score 58.5; DB 1; Length 347;
Best Local Similarity 52.2%; Pred. No. 0.73;
Matches 12; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 KPDELDYNDIEKKICKMEKCS 23
| : : | : : : | : : : | : : |
DB 304 KKAEDTLE-DIDTEICKMDKCS 325

RESULT 13
CSP_PLAYO STANDARD; PRT; 367 AA.
ID CSP_PLAYO
AC P06914;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
OS Plasmodium berghei yoelli.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OC NCBI_TaxID=5862;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87137555; PubMed=3102479;
RA Lal A.A., de la Cruz V.F., Welsh J.A., Charoenvit Y., Maloy W.L.,
RA McCutchan T.F.
RT "Structure of the gene encoding the circumsporozoite protein of
RT Plasmodium yoelli. A rodent model for examining antimalarial
RT sporozoite vaccines."
RL J. Biol. Chem. 262:2937-2940(1987).
RN [2]
RP SEQUENCE OF 1-140 AND 260-367 FROM N.A.
RX MEDLINE=88232798; PubMed=3287156;
RA de la Cruz V.F., Lal A.A., McCutchan T.F.;
RA "Variation among circumsporozoite protein genes from rodent
RA Malarias."
RT Mol. Biochem. Parasitol. 28:31-38(1988).
CC -I- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT
CC SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
CC MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
CC VETERINATE HOST).
CC -I- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR
CC ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES
CC WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
CC -I- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
CC -----
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CC -----
DR EMBL: J02695; AAA29558.1; -
DR EMBL: M18821; AAA29559.1; -
DR EMBL: M22698; AAA29560.1; -

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DR   PIR: A26271; OZKOMY.
DR   InterPro: IPR003057; Crcmsprzoite.
DR   InterPro: IPR000884; TSP1.
DR   Pfam: PF00090; tsp_1; 1.
DR   PRINTS: PR01303; CRCMSPRZOITE.
DR   SMART: SM00209; TSP1; 1.
KW   Malaria; Sporozoite; Repeat; Signal.
FT   SIGNAL          1      19
FT   CHAIN           20     367
FT   DOMAIN          139    228
FT   DOMAIN          229    260
SQ   SEQUENCE        367 AA; 38888 MW; 1EAS6AFFFCB5E3 CRC64;
Oy       1 KPKDELVDENDIEKKICKMKCS 23
         | : | | | ||: ::|||::|||
Db       324 KQENLTLE-DIDTEICMDKCS 345

RESULT  14
3HAO_YEAST
ID       3HAO_YEAST      STANDARD:      PRT:   177 AA.
AC       PA7096;
DT       01-FEB-1996 (Rel. 33, Created)
DT       01-FEB-1996 (Rel. 33, Last sequence update)
DT       15-JUL-1999 (Rel. 38, Last annotation update)
DE       3-HYDROXYANTHRANILATE 3,4-DIOXYGENASE [EC 1.13.11.6] (3-HAO)
DE       (3-HYDROXYANTHRANILIC ACID DIOXYGENASE) (3-HYDROXYANTHRANILATE
DE       OXYGENASE).
GN       BNAI OR YJR025C OR J1550.
OS       Saccharomyces cerevisiae (Baker's yeast).
OC       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC       Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX       NCBI_TaxID=4932;
RX       [1]
RX       SEQUENCE FROM N.A.
RX       MEDLINE=96109930; PubMed=8619316;
RA       Zagulski M., Babinska B., Gromadka R., Migdalski A., Rytko J.,
RA       Sulicka J., Herbert C.J.;
RT       "The sequence of 24.3 kb from chromosome X reveals five complete open
RT       reading frames, all of which correspond to new genes, and a tandem
RT       insertion of a Ty1 transposon.";
RL       Yeast 11:1179-1186(1995).
CC       [2]
CC       CHARACTERIZATION.
CC       MEDLINE=96196537; PubMed=9539135;
CC       Kucharczyk R., Zagulski M., Rytko J., Herbert C.J.;
CC       "The yeast gene YJR025C encodes a 3-hydroxyanthranilic acid
CC       dioxygenase and is involved in nicotinic acid biosynthesis.";
CC       FEBS Lett. 424:127-130(1998).
CC       -1- CATALYTIC ACTIVITY: 3-HYDROXYANTHRANILATE + O(2) = 2-AMINO-3-
CC       CARBOXYMYCONATE SEMIALDEHYDE.
CC       -1- COFACTOR: FERROUS ION.
CC       -1- PATHWAY: INVOLVED IN NICOTINIC ACID BIOSYNTHESIS.
CC       -1- SIMILARITY: STRONG, TO MAMMALIAN 3-HYDROXYANTHRANILATE 3,4-
CC       DIOXYGENASE.
CC       -----
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CC       or send an email to license@isb-sib.ch).
CC       -----
CC       EMBL: Z49525; CAA89550.1; -.
CC       EMBL: X87297; CAA60720.1; -.
CC       SCD; S0003786; BNAI.
CC       Oxidoreductase, Dioxygenase; Iron.
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50 SEQUENCE 1177 AA; 20235 MW; 930D69F466322417 CRC64;
Query Match 41.7%; Score 53; DB 1; Length 177;
Best Local Similarity 66.7%; Pred. No. 2.1;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 6 LDYENDIEKKTIC 17
11:111111:11:1
Db 152 LDFENDVEKRTIC 163

RESULT 15
CSP_PLAYS
ID CSP_PLAYS STANDARD: PRT: 343 AA.
AC P13826;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CIRCUMSPOROZOITE PROTEIN (CS) (FRAGMENT).
OS Plasmodium vivax (strain Salvador I).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5856;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=66070222; PubMed=2416057;
RA McCutchan T.F., Lal A.A., de la Cruz V.F., Miller L.H., Maloy W.L.,
RA Chaoeavit Y., Beaudoin R.L., Guerry P., Wistar R. Jr., Hoffman S.L.,
RA Hockmeyer W.T., Collins M.E., Wirth D.;
RT "Sequence of the immunodominant epitope for the surface protein on
RL sporozoites of Plasmodium vivax."
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87194878; PubMed=2437120;
RA de la Cruz V.F., Lal A.A., Welsh J.A., McCutchan T.F.;
RT "Evolution of the immunodominant domain of the circumsporozoite
RT protein gene from Plasmodium vivax. Implications for vaccines."
RN J. Biol. Chem. 262:6464-6467(1987).
CC -!- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT
CC SURFACE ANTIGEN ON THE SPOOROITE (THE INFECTIVE STAGE OF THE
CC MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
CC VERTEBRATE HOST).
CC -!- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR
CC ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES
CC WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
CC -!- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
CC Interpro: IPR0000884; TSP1.
DR Pfam: PF00090; TSP_1; 1.
DR SMART: SM00209; TSP1; 1.
DR PROSITE: PS50092; TSP1; 1.
KW Sporozoite; Malaria; Repeat.
FT NON_TER 1
FT DOMAIN 63 243 19 X 9 AA TAMDEM REPEATS OF P-G-D-R-A-D-
FT FT G-O-P.
FT SEQUENCE 343 AA; 34155 MW; 308EFD5BC15DFC3 CRC64;

Query Match 40.2%; Score 51; DB 1; Length 343;
Best Local Similarity 43.5%; Pred. No. 7.3;
Matches 10; Conservative 5; Mismatches 6; Indels 2; Gaps 1;

OY 1 KPKDELVDYENDIEKKTICKMEKS 23
11:111111:11:111111:
Db 301 KPEDLT--LNDIETDVCYTMCKCA 321

Search completed: January 29, 2002, 11:13:39
Job time: 815 sec

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ID Q90P8 PRELIMINARY; PRT; 80 AA.  
 AC Q90P8;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CIRCUMSPOROZOITE PROTEIN (FRAGMENT).  
 GN CS.  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 NCBI\_TaxID=5833;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-M4;  
 RA de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;  
 "Sequence variation in the non-repeat region of the Plasmodium  
 falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and  
 RT Burmese field isolates and from laboratory strains."  
 RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AJ269957; CAB64237.1; -.  
 DR InterPro: IPR003067; Circsprzoite.  
 DR Pfam: PF00090; tsp\_1; 1.  
 DR PRINTS: PR01303; CRCMSPRZOITE.  
 DR SMART: SM00209; TSP1; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 80 80  
 SQ SEQUENCE 80 AA; 9073 MW; ABF404B8FB142B1E CRC64;

Query Match 100.0%; Score 127; DB 5; Length 80;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KPKELDYENDIEKKICKMEKS 23  
 Db 50 KPKELDYENDIEKKICKMEKS 72

RESULT 3  
 ID Q90P7 PRELIMINARY; PRT; 80 AA.  
 AC Q90P7;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CIRCUMSPOROZOITE PROTEIN (FRAGMENT).  
 GN CS.  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 NCBI\_TaxID=5833;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-D4230;  
 RA de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;  
 "Sequence variation in the non-repeat region of the Plasmodium  
 falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and  
 RT Burmese field isolates and from laboratory strains."  
 RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AJ269961; CAB64180.1; -.  
 DR InterPro: IPR000884; TSP1.  
 DR Pfam: PF00090; tsp\_1; 1.  
 DR PRINTS: PR01303; CRCMSPRZOITE.  
 DR SMART: SM00209; TSP1; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 80 80  
 SQ SEQUENCE 80 AA; 9047 MW; BA769C90DB031C3E CRC64;

Query Match 100.0%; Score 127; DB 5; Length 80;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KPKELDYENDIEKKICKMEKS 23  
 Db 50 KPKELDYENDIEKKICKMEKS 72

RESULT 4  
 ID Q90P3 PRELIMINARY; PRT; 80 AA.  
 AC Q90P3;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CIRCUMSPOROZOITE PROTEIN (FRAGMENT).  
 GN CS.  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 NCBI\_TaxID=5833;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-D4405;  
 RA de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;  
 "Sequence variation in the non-repeat region of the Plasmodium  
 falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and  
 RT Burmese field isolates and from laboratory strains."  
 RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AJ269969; CAB64188.1; -.  
 DR InterPro: IPR000884; TSP1.  
 DR Pfam: PF00090; tsp\_1; 1.  
 DR PRINTS: PR01303; CRCMSPRZOITE.  
 DR SMART: SM00209; TSP1; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 80 80  
 SQ SEQUENCE 80 AA; 9033 MW; BA71EBEDDB03193B CRC64;

Query Match 100.0%; Score 127; DB 5; Length 80;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KPKELDYENDIEKKICKMEKS 23  
 Db 50 KPKELDYENDIEKKICKMEKS 72

RESULT 5  
 ID Q90P1 PRELIMINARY; PRT; 80 AA.  
 AC Q90P1;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CIRCUMSPOROZOITE PROTEIN (FRAGMENT).  
 GN CS.  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 NCBI\_TaxID=5833;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-B1896;  
 RA de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;  
 "Sequence variation in the non-repeat region of the Plasmodium  
 falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and  
 RT Burmese field isolates and from laboratory strains."  
 RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AJ269978; CAB64197.1; -.  
 DR InterPro: IPR003067; Circsprzoite.  
 DR Pfam: PF00090; tsp\_1; 1.  
 DR PRINTS: PR01303; CRCMSPRZOITE.  
 DR SMART: SM00209; TSP1; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 80 80

SO SEQUENCE 80 AA: 9102 MW: BFC6C970CEFOFA3E CRC64;  
Query Match 100.0%; Score 127; DB 5; Length 80;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 KPKDELDYENDIEKKICKMEKCS 23  
DB 50 KPKDELDYENDIEKKICKMEKCS 72  
RESULT 6  
O9TVN9 PRELIMINARY: PRT: 80 AA.  
AC O9TVN9:  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE CIRCUMSPOROZOITE PROTEIN (FRAGMENT).  
GN CS.  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=M0, M6, M7, AND M1;  
RA de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;  
RT "Sequence variation in the non-repeat region of the Plasmodium  
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and  
RT Burmese field isolates and from laboratory strains."  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ269955; CAB64242.1; -  
DR EMBL: AJ269958; CAB64238.1; -  
DR EMBL: AJ269959; CAB64239.1; -  
DR EMBL: AJ269956; CAB64241.1; -  
DR InterPro: IPR000884; TSP1.  
DR InterPro: IPR003067; Circmsprzoite.  
DR Pfam: PF00090; tsp\_1; 1  
DR PRINTS: PR01303; CRCMSPRZOITE.  
DR SMART: SM00209; TSP1; 1.  
FT NON\_TER 1  
FT SEQUENCE 80 AA: 9074 MW: ABF40C90DBIC033E CRC64;  
SO  
Query Match 100.0%; Score 127; DB 5; Length 80;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 KPKDELDYENDIEKKICKMEKCS 23  
DB 50 KPKDELDYENDIEKKICKMEKCS 72  
RESULT 7  
O9TVN9 PRELIMINARY: PRT: 80 AA.  
AC O9TVN9:  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE CIRCUMSPOROZOITE PROTEIN (FRAGMENT).  
GN CS.  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B1893, B1804, B1853, B1870, B1872, B1881, AND B1882;  
RA de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;  
RT "Sequence variation in the non-repeat region of the Plasmodium  
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and

RT Burmese field isolates and from laboratory strains."  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ269977; CAB64196.1; -  
DR EMBL: AJ269971; CAB64190.1; -  
DR EMBL: AJ269972; CAB64191.1; -  
DR EMBL: AJ269973; CAB64192.1; -  
DR EMBL: AJ269974; CAB64193.1; -  
DR EMBL: AJ269975; CAB64194.1; -  
DR EMBL: AJ269976; CAB64195.1; -  
DR InterPro: IPR000884; TSP1.  
DR InterPro: IPR003067; Circmsprzoite.  
DR Pfam: PF00090; tsp\_1; 1.  
DR PRINTS: PR01303; CRCMSPRZOITE.  
DR SMART: SM00209; TSP1; 1.  
FT NON\_TER 1  
FT SEQUENCE 80 AA: 9074 MW: ADF10C8FCA1C1924 CRC64;  
SO  
Query Match 100.0%; Score 127; DB 5; Length 80;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 KPKDELDYENDIEKKICKMEKCS 23  
DB 50 KPKDELDYENDIEKKICKMEKCS 72  
RESULT 8  
O9TVN7 PRELIMINARY: PRT: 115 AA.  
AC O9TVN7:  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE CIRCUMSPOROZOITE PROTEIN (FRAGMENT).  
GN CSP.  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=815, 947, AND 808;  
RX MEDLINE=95077069; PubMed=7985759;  
RA Jongwutives S., Tanabe K., Hughes M.K., Kanbara H., Hughes A.L.;  
RT "Allelic variation in the circumsporozoite protein of Plasmodium  
falciparum from Thai field isolates."  
RL Am. J. Trop. Med. Hyg. 51:659-668(1994).  
DR EMBL: M83153; AAA29566.1; -  
DR EMBL: M83171; AAA29549.1; -  
DR EMBL: M83151; AAA29564.1; -  
DR InterPro: IPR000884; TSP1.  
DR InterPro: IPR003067; Circmsprzoite.  
DR Pfam: PF00090; tsp\_1; 1.  
DR PRINTS: PR01303; CRCMSPRZOITE.  
DR SMART: SM00209; TSP1; 1.  
FT NON\_TER 1  
FT SEQUENCE 115 AA: 12925 MW: 697DF63EBEBDA90 CRC64;  
SO  
Query Match 100.0%; Score 127; DB 5; Length 115;  
Best Local Similarity 100.0%; Pred. No. 1.5e-09;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 KPKDELDYENDIEKKICKMEKCS 23  
DB 71 KPKDELDYENDIEKKICKMEKCS 93  
RESULT 9  
O27425 PRELIMINARY: PRT: 424 AA.  
ID O27425  
AC O27425;

```
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE CIRCUMSPOROZOITE PROTEIN.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=844;
RX MEDLINE=84250215; PubMed=6204383;
RA Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
RA Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,
RA Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
RT "Structure of the gene encoding the immunodominant surface antigen on
RT the sporozoite of the human malaria parasite Plasmodium falciparum.";
RL Science 225:593-599(1984).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=844;
RA la Cruz V.F.;
RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=844;
RX Jongwutlives S., Tanabe K., Kanbara H.;
RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M83169; AAA29547.1; -.
DR EMBL; M83149; AAA29562.1; -.
DR InterPro: IPR003067; Crcmsprzoite.
DR InterPro: IPR003067; Crcmsprzoite.
DR Pfam: PF00090; tsp_1; 1.
DR Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
DR PRINTS; PR01303; CRCMSPRZOITE.
DR SMART; SM00209; TSP1; 1.
SQ SEQUENCE 424 AA; 45592 MW; F20CEB60636DB98E CRC64;

Query Match 100.0%; Score 127; DB 5; Length 424;
Best Local Similarity 100.0%; Pred. No. 5e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPKDELDYENDIEKTKCKMEKCS 23
DB 380 KPKDELDYENDIEKTKCKMEKCS 402

RESULT 10
OY 099256 PRELIMINARY; PRT; 424 AA.
AC 099256;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE CIRCUMSPOROZOITE PROTEIN (CS) PRECURSOR, VARIANT 2 (FRAGMENT).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=91270295; PubMed=2052038;
RX Lockyer M.J.;
RA "Clonal variation in the Plasmodium falciparum circumsporozoite
RT protein gene.";
RL Mol. Biochem. Parasitol. 45:179-182(1991).
CC -1- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT
CC SURFACE ANTIGEN ON THE SPOROZOITE (THE INECTIVE STAGE OF THE
CC MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
CC VERTEBRATE HOST).
CC -1- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR
CC ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES
CC WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
DR EMBL; M57499; AAA63422.1; -.
```

```
DR InterPro: IPR000884; TSP1.
DR InterPro: IPR003067; Crcmsprzoite.
DR Pfam: PF00090; tsp_1; 1.
DR PRINTS; PR01303; CRCMSPRZOITE.
DR SMART; SM00209; TSP1; 1.
KW Malaria; Repeat; Sporozoite; Signal.
FT SIGNAL 1 16 BY SIMILARITY.
FT CHAIN 17 >424 CIRCUMSPOROZOITE PROTEIN.
FT DOMAIN 123 302 4-RESIDUE TANDEM REPEATS.
FT NON_TER 424 424
FT SEQUENCE 424 AA; 45609 MW; BFD0F906C664B8F CRC64;

Query Match 100.0%; Score 127; DB 5; Length 424;
Best Local Similarity 100.0%; Pred. No. 5e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPKDELDYENDIEKTKCKMEKCS 23
DB 380 KPKDELDYENDIEKTKCKMEKCS 402

RESULT 11
OY 027246 PRELIMINARY; PRT; 432 AA.
AC 027246;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE CIRCUMSPOROZOITE PROTEIN.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=946;
RX Jongwutlives S., Tanabe K., Kanbara H.;
RA Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
RA Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,
RA Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
RT "Structure of the gene encoding the immunodominant surface antigen on
RT the sporozoite of the human malaria parasite Plasmodium falciparum.";
RL Science 225:593-599(1984).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=946;
RX Jongwutlives S., Tanabe K., Kanbara H.;
RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M83155; AAA29568.1; -.
DR EMBL; M83170; AAA29548.1; -.
DR EMBL; M83152; AAA29565.1; -.
DR EMBL; M83158; AAA29571.1; -.
DR EMBL; M83166; AAA29544.1; -.
DR EMBL; M83168; AAA29546.1; -.
DR InterPro: IPR000884; TSP1.
DR InterPro: IPR003067; Crcmsprzoite.
DR Pfam: PF00090; tsp_1; 1.
DR PRINTS; PR01303; CRCMSPRZOITE.
DR SMART; SM00209; TSP1; 1.
SQ SEQUENCE 432 AA; 46414 MW; 8787E6005578873A CRC64;

Query Match 100.0%; Score 127; DB 5; Length 432;
Best Local Similarity 100.0%; Pred. No. 5.1e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPKDELDYENDIEKTKCKMEKCS 23
```



Db 388 KPDELVDYNDIEKKICKMEKCS 410

# RESULT 12

ID 025827 PRELIMINARY; PRT: 432 AA.

AC 025827;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE CIRCUMSPOROZOITE PROTEIN.

GN CSP.

OS Plasmodium falciparum.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI\_TaxID=5633;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=838;

RX MEDLINE=84250215; PubMed=6204383;

RA Dame J.B., Williams J.L., McCutchan J.F., Weber J.L., Wirtz R.A.,

Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,

Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;

RT "Structure of the gene encoding the immunodominant surface antigen on

the sporozoite of the human malaria parasite Plasmodium falciparum.";

RL Science 225:593-599(1984).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=838;

RA la Cruz V.F.;

RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=838;

RA Jongwutlives S., Tanabe K., Kanbara H.;

RL Mol. Biochem. Parasitol. 0:0-0(0).

DR EMBL: M83165; AAA29543.1;

DR InterPro: IPR000884; TSP1.

DR InterPro: IPR003067; Circsprztoite.

DR Pfam: PF00090; tsp\_1; 1.

DR PRINTS: PR01303; CRCMSPRZOITE.

DR SMART: SM00209; TSP1; 1.

DR SEQUENCE 432 AA; 46385 MW; 2CB8D9A68E11945F CRC64;

OY 1 KPDELVDYNDIEKKICKMEKCS 23

Db 388 KPDELVDYNDIEKKICKMEKCS 410

Query Match 100.0%; Score 127; DB 5; Length 432;

Best Local Similarity 100.0%; Pred. No. 5.1e-09;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

# RESULT 13

ID 090001 PRELIMINARY; PRT: 80 AA.

AC 090001;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE CIRCUMSPOROZOITE PROTEIN (FRAGMENT).

GN CS.

OS Plasmodium falciparum (isolate K1 / Thailand).

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI\_TaxID=5633;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K1;

RA de Stricker K., Vuust J., Jepsen S., Oeuvaray C., Theisen M.;

RT "Sequence variation in the non-repeat region of the Plasmodium

falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and

Burmese field isolates and from laboratory strains.";

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ269946; CAB64171.1;

DR InterPro: IPR000884; TSP1.

DR InterPro: IPR003067; Circmsprztoite.

DR Pfam: PF00090; tsp\_1; 1.

DR PRINTS: PR01303; CRCMSPRZOITE.

DR PROSITE: PS50092; TSP1; 1.

DR SMART: SM00209; TSP1; 1.

FT NON\_TER 1 1

FT NON\_TER 80 80

FT SEQUENCE 80 AA; 9137 MW; 4204EBC68F0B1434 CRC64;

Query Match 97.6%; Score 124; DB 5; Length 80;

Best Local Similarity 95.7%; Pred. No. 2.7e-09;

Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPDELVDYNDIEKKICKMEKCS 23

Db 50 KPDELVDYNDIEKKICKMEKCS 72

Query Match 97.6%; Score 124; DB 5; Length 80;

Best Local Similarity 95.7%; Pred. No. 2.7e-09;

Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPDELVDYNDIEKKICKMEKCS 23

Db 50 KPDELVDYNDIEKKICKMEKCS 72

Query Match 97.6%; Score 124; DB 5; Length 80;

Best Local Similarity 95.7%; Pred. No. 2.7e-09;

Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPDELVDYNDIEKKICKMEKCS 23

Db 50 KPDELVDYNDIEKKICKMEKCS 72

Query Match 97.6%; Score 124; DB 5; Length 80;

Best Local Similarity 95.7%; Pred. No. 2.7e-09;

Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPDELVDYNDIEKKICKMEKCS 23

Db 50 KPDELVDYNDIEKKICKMEKCS 72

Query Match 97.6%; Score 124; DB 5; Length 80;

Best Local Similarity 95.7%; Pred. No. 2.7e-09;

Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPDELVDYNDIEKKICKMEKCS 23

Db 50 KPDELVDYNDIEKKICKMEKCS 72

Query Match 97.6%; Score 124; DB 5; Length 80;

Best Local Similarity 95.7%; Pred. No. 2.7e-09;

Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPDELVDYNDIEKKICKMEKCS 23

Db 50 KPDELVDYNDIEKKICKMEKCS 72

Query Match 97.6%; Score 124; DB 5; Length 80;

Best Local Similarity 95.7%; Pred. No. 2.7e-09;

Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPDELVDYNDIEKKICKMEKCS 23

Db 50 KPDELVDYNDIEKKICKMEKCS 72

Query Match 97.6%; Score 124; DB 5; Length 80;

Best Local Similarity 95.7%; Pred. No. 2.7e-09;

Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPDELVDYNDIEKKICKMEKCS 23

Db 50 KPDELVDYNDIEKKICKMEKCS 72

Query Match 97.6%; Score 124; DB 5; Length 80;

Best Local Similarity 95.7%; Pred. No. 2.7e-09;

Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPDELVDYNDIEKKICKMEKCS 23

Db 50 KPDELVDYNDIEKKICKMEKCS 72

Query Match 97.6%; Score 124; DB 5; Length 80;

Best Local Similarity 95.7%; Pred. No. 2.7e-09;

Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPDELVDYNDIEKKICKMEKCS 23

Db 50 KPDELVDYNDIEKKICKMEKCS 72

Query Match 97.6%; Score 124; DB 5; Length 80;

Best Local Similarity 95.7%; Pred. No. 2.7e-09;

Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPDELVDYNDIEKKICKMEKCS 23

Db 50 KPDELVDYNDIEKKICKMEKCS 72

Query Match 97.6%; Score 124; DB 5; Length 80;

Best Local Similarity 95.7%; Pred. No. 2.7e-09;

OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1;  
RA de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;  
RT "Sequence variation in the non-repeat region of the plasmodium  
RT falciparum glutamate rich protein (GLRP) from Brazil, Senegalese, and  
RT Burmese field isolates and from laboratory strains."  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ269951; CAB64176.1; -  
DR InterPro: IPR003067; Crmsprzoite.  
DR Pfam: PF00090; tsp\_1; 1.  
DR PRINTS: PR01303; CRGMSPRZOITE.  
DR SMART: SM00209; TSP1; 1.  
FT NON\_TER 1  
FT NON\_TER 80  
SQ SEQUENCE 80 AA: 9032 MW: ADED6F0E266AD98E CRC64;

Query Match 97.6%; Score 124; DB 5; Length 80;  
Best Local Similarity 95.7%; Pred. No. 2.7e-09;  
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KPREDLDYENDIEKKICKMEKCS 23  
||||:|||||||||||||||||  
DB 50 KPRDQLDYENDIEKKICKMEKCS 72

Search completed: January 29, 2002, 11:12:10  
Job time: 766 sec



XX Novel recombinant protein as vaccine for treating malarial infection  
 PT comprises antigenic peptides obtained from different stages of  
 PT Plasmodium falciparum life cycle  
 PS  
 XX Claim 2; Page 16; 52pp; English.  
 CC The present sequence is the antigenic epitope p594, derived from  
 CC circumsporozoite protein (CSP) of the sporozoite stage of Plasmodium  
 CC falciparum. It is used in the construction of recombinant protein.  
 CC CDC/NIMAIIVAC-1, which is a multivalent, multistage malarial vaccine.  
 CC The recombinant protein comprises, melittin signal peptide, (His)<sub>6</sub> tag,  
 CC T-cell epitope from tetanus toxoid and 21 antigenic epitopes from  
 CC circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2),  
 CC liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1),  
 CC MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175  
 CC (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific  
 CC antigen, Pf27. These epitopes were obtained at different stages of the  
 CC life cycle of P. falciparum. CDC/NIMAIIVAC-1 vaccine has antiparasitic  
 CC activity and can be used for treatment and prevention of malarial  
 CC infections. Anti-CDC/NIMAIIVAC-1 antibodies can be used for detecting  
 CC P. falciparum in biological samples.  
 CC  
 XX  
 SQ Sequence 21 AA:

Query Match 100.0%; Score 109; DB 21; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4,4e-10;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 DIEKKICKMEKCSVFNVVNS 21  
 DB 1 diekkickmekscsvfnvns 21  
 ||||||||||||||||

RESULT 2  
 AAR13175 AAR13175 standard; protein; 309 AA.  
 ID AAR13175  
 XX  
 AC AAR13175;  
 XX  
 DT 29-AUG-1991 (first entry)  
 XX  
 DE NS1\_81-RLfdelta9.  
 XX  
 KW Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;  
 KW hybrid; influenza virus; non-structural protein 1; fusion.  
 XX  
 OS Plasmodium falciparum.  
 OS Influenza virus (A/PK/8/34/).

XX  
 FH Key Location/Qualifiers  
 FT 1..81  
 FT /label= "N-terminal of NS1  
 FT /note= "Influenza virus nonstructural protein 1"  
 FT 82..87  
 FT /label= synthetic linker  
 FT 88  
 FT /label= artifact  
 FT /note= "see comments"  
 FT 89..193  
 FT /label= AAS 19-123 of CS protein  
 FT /note= "Region 1 contg. flanking region less  
 FT 194..309  
 FT /label= AAS 297-412 of CS protein  
 FT /note= "Region II flanking region minus 9 N-term-  
 FT inal AAS"  
 FT  
 PN EP432965-A.  
 XX  
 XX  
 PD 19-JUN-1991.  
 XX

PF 06-DEC-1990; 90EP-0313257.  
 XX  
 PR 08-DEC-1989; 89US-0447746.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM.  
 PA (USA ) US SEC OF THE ARMY.  
 PA (BIOM-) BIOMEDICAL RES INST.  
 XX  
 PI Gross MS, Gordon DM, Hollingdale MR;  
 XX  
 DR WPI; 1991-179771/25.  
 XX  
 PT Polypeptide comprising immunogenic determinants from P falciparum  
 PT - for vaccine against malaria infection in humans.  
 PS  
 XX Example 1; Page 7; 18pp; English.

CC The polypeptide is prepd. by genetic engineering of genes encoding  
 CC the P. falciparum circumsporozoite (CS) protein [Dane et al.,  
 CC Science 225 : 593 (1984)], and the influenza virus non-structural  
 CC protein 1 (NS1), [Baez et al., Nucleic Acids Research, 8 : 5845  
 CC (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NS1  
 CC (NS1\_81) is linked via a synthetic sequence to DNA encoding Region  
 CC I contg. flanking regionless the 18 AA signal region, which in  
 CC turn is fused to DNA encoding Region II-contg. flanking region  
 CC less the first nine N-terminal AAs. This CS fusion is designated  
 CC RLfdelta9. The Pro residue separating the Asp (at the C-terminal  
 CC of the linker) from RLfdelta9 is an artifact of a filled in BamHI  
 CC site. The peptide can be used in a vaccine for protection against  
 CC malaria.  
 CC See also AAR12306-RL2311 and AAR13176-RL3179.  
 CC  
 XX  
 SQ Sequence 309 AA:

Query Match 100.0%; Score 109; DB 12; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 7,1e-09;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 DIEKKICKMEKCSVFNVVNS 21  
 DB 275 diekkickmekscsvfnvns 295  
 ||||||||||||||||

RESULT 3  
 AAR07945 AAR07945 standard; protein; 319 AA.  
 ID AAR07945  
 XX  
 AC AAR07945;  
 XX  
 DT 22-FEB-1991 (first entry)  
 XX  
 DE NS181RLFauth plasmid product.  
 XX  
 KW Malaria; vaccine.  
 XX  
 OS Plasmodium falciparum.

XX  
 FH Key Location/Qualifiers  
 FT 1..81  
 FT /label= NS181 protein fragment  
 FT /note= "from plasmid pmG-1"  
 FT 89..193  
 FT /label= Fragment of circumsporozoite protein  
 FT 204..319  
 FT /label= Fragment of circumsporozoite protein  
 FT  
 PN EP398540-A.  
 XX  
 XX  
 PD 22-NOV-1990.  
 XX  
 PF 01-MAY-1990; 90EP-0304720.  
 XX

PR	03-MAY-1989;	89US-0346863.
XX		
PA	(SMIK ) SMITHKLINE BEECHAM.	
XX		
PI	Gross MS, Young JF:	
XX		
DR	WPI: 1990-350299/47.	
DR	N-PsDB: AAQ06580.	
XX		
PT	New polypeptide used in malaria vaccine - comprises immunogenic	
PT	determinants from 1st and 2nd flanking regions of plasmodium	
PT	surface protein and intermediate repeat domain	
XX		
PS	Example 2; Page 11-12; 24pp: English.	
XX		
CC	The product is useful in preparation of vaccines for treatment and	
CC	prophylaxis of plasmodium sporozite infection. It may be easily	
CC	produced in large pure quantities from a transformed E.coli	
CC	expression system.	
XX		
SQ	Sequence 319 AA;	
OY	Query Match 100.0%; Score 109; DB 11; Length 319; Best Local Similarity 100.0%; Pred. No. 7.4e-09; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  1 DIEKKICKMEKCSVFNVVNS 21       Db 285 diekkickmekcsvfnnvns 305	
RESULT 4		
AAR13176		
ID AAR13176	standard; Protein; 319 AA.	
XX		
AC AAR13176;		
XX		
D7 29-AUG-1991	(first entry)	
XX		
DE NSL_81-RLFAuth.		
XX		
KW Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;		
RW hybrid; Influenza virus; non-structural protein 1; fusion.		
XX		
OS Plasmodium falciparum.		
OS Influenza virus (A/PR/8/34).		
XX		
FH Key Location/Qualifiers		
FT Region 1..81	/label= N-terminal of NSI	
FT Peptide 82..87	/note= "Influenza virus nonstructural protein 1"	
FT Region 88	/label= synthetic linker	
FT Region 89..193	/label= artifact	
FT Region /note= "see comments"		
FT Region /label= AAs 19-123 of CS protein		
FT Region /note= "Region I contg. flanking region less		
FT Region 194	/label= artifact	
FT Region /note= "see comments"		
FT Region 195..319	/label= AAs 288-412 of CS protein	
FT Region /note= "Region II flanking region"		
XX		
PN EPA32965-A.		
XX		
PD 19-JUN-1991.		
XX		
PE 06-DEC-1990;	90EP-0313257.	

[illegible]

```

FT      /note="Region I contg. flanking region less
FT      signal sequence"
FT      Region
FT      194..201
FT      /label="immunodominant repeat region"
FT      /note="two tetrapeptide repeat units"
FT      Region
FT      202
FT      /label="artifact"
FT      /note="see comments"
FT      203..327
FT      /label="AAs 288-412 of CS protein"
FT      /note="Region II flanking region"
FT
FT
FT      EP432965-A.
FT      19-JUN-1991.
FT
FT      06-DEC-1990; 90EP-0313257.
FT
FT      08-DEC-1989; 89US-0447746.
FT
FT      (SMIK ) SMITHKLINE BEECHAM.
FT      (USSA ) US SEC OF THE ARMY.
FT      (BIOM-) BIOMEDICAL RES INST.
FT
FT      Gross MS, Gordon DM, Hollingdale MR;
FT      WPI; 1991-179771/25.
FT
FT      Polypeptide comprising immunogenic determinants from P falciparum
FT      - for vaccine against malaria infection in humans.
FT
FT      Example 3; Page 10; 18pp; English.
FT
FT      The polypeptide is prepd. by genetic engineering of genes encoding
FT      the P. falciparum circumsporozoite (CS) protein [Dane et al.,
FT      Science 225 : 593 (1984)] and the influenza virus non-structural
FT      protein 1 (NS1), [Baez et al., Nucleic Acids Research, 8 : 5845
FT      (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NS1
FT      (NS1.81) is linked via a synthetic sequence to DNA encoding Region
FT      I contg. flanking region less the 18 AA signal region. This is
FT      linked to a synthetic sequence encoding two repeat units from the
FT      immunodominant region, which in turn is fused to DNA encoding
FT      Region II contg. flanking region. The Pro residue separating the
FT      Asp (at the C-terminal of the linker) from the Region I-contg. CS
FT      flanking region is an artifact of a filled-in BamHI site; the Gly
FT      separating the repeat units and the Region II-contg. CS flanking
FT      region is an artifact of a synthetic FokI/ThiIII I linker. The
FT      peptide can be used in a vaccine for protection against malaria.
FT      See also AAR12306-R12311 and AAR13175-R13179.
FT
FT      Sequence 327 AA;
FT
FT      Query Match 100.0%; Score 109; DB 12; Length 327;
FT      Best Local Similarity 100.0%; Pred. No. 7.5e-09;
FT      Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT
FT      1 DIEKRICMEKCSVFNVNS 21
FT      ||||||||||||||||
FT      Db 293 diekricmekcsvfnvns 313
FT
FT      RESULT 6
FT      AAR13178
FT      ID AAR13178 standard; Protein: 335 AA.
FT
FT      AAR13178;
FT
FT      29-AUG-1991 (first entry)
FT
FT      NS1_81(NANP)4RLfAuth.
FT
FT      Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;

```

```

KW      hybrid; influenza virus; non-structural protein 1; fusion.
XX
XX      Plasmodium falciparum.
OS
OS      Influenza virus (A/PR/8/34).
XX
XX      Key
FH      Location/Qualifiers
FT      1..81
FT      /label="N-terminal of NS1"
FT      /note="Influenza virus nonstructural protein 1"
FT      82..97
FT      /label="immunodominant repeat region"
FT      /note="four tetrapeptide repeat units"
FT      98..103
FT      /label="synthetic linker"
FT      104
FT      /label="artifact"
FT      /note="see comments"
FT      105..209
FT      /label="AAs 19-123 of CS protein"
FT      /note="Region I contg. flanking region less
FT      signal sequence"
FT      Region
FT      210
FT      /label="artifact"
FT      /note="see comments"
FT      211..335
FT      /label="AAs 288-412 of CS protein"
FT      /note="Region II flanking region"
FT
FT      EP432965-A.
FT      19-JUN-1991.
FT
FT      06-DEC-1990; 90EP-0313257.
FT
FT      08-DEC-1989; 89US-0447746.
FT
FT      (SMIK ) SMITHKLINE BEECHAM.
FT      (USSA ) US SEC OF THE ARMY.
FT      (BIOM-) BIOMEDICAL RES INST.
FT
FT      Gross MS, Gordon DM, Hollingdale MR;
FT      WPI; 1991-179771/25.
FT
FT      Polypeptide comprising immunogenic determinants from P falciparum
FT      - for vaccine against malaria infection in humans.
FT
FT      Example 4; Page 11; 18pp; English.
FT
FT      The polypeptide is prepd. by genetic engineering of genes encoding
FT      the P. falciparum circumsporozoite (CS) protein [Dane et al.,
FT      Science 225 : 593 (1984)] and the influenza virus non-structural
FT      protein 1 (NS1), [Baez et al., Nucleic Acids Research, 8 : 5845
FT      (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NS1
FT      (NS1.81) is linked to a synthetic sequence encoding four repeat
FT      units from the immunodominant region, which in turn is linked via
FT      a synthetic sequence to DNA encoding Region I contg. flanking
FT      region less the 18 AA signal region. This is linked to DNA
FT      encoding Region II-contg. flanking region. The Pro residue sep-
FT      arating the Asp (at the C-terminal of the linker) from the Region
FT      I-contg. CS flanking region is an artifact of a filled-in BamHI
FT      site; the Gly separating the Region I and II-contg. CS flanking
FT      regions is an artifact of a synthetic FokI/ThiIII I linker. The
FT      peptide can be used in a vaccine for protection against malaria.
FT      See also AAR12306-R12311 and AAR13175-R13179.
FT
FT      Sequence 335 AA;
FT
FT      Query Match 100.0%; Score 109; DB 12; Length 335;
FT      Best Local Similarity 100.0%; Pred. No. 7.7e-09;
FT      Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 DIEKICKMEKCSSVFNVNS 21
        ||||||||||||||||
DB      301 diekickmekcssvfnvns 321

RESULT  7
AAR13179
ID      AAR13179 standard; Protein: 335 AA.
XX
AC      AAR13179;
XX
DT      29-AUG-1991 (first entry)
XX
DE      NS1_81(NVDP)4RLfAuth.
XX
KM      Immunogenic determinant: circumsporozoite; CS; vaccine: malaria;
XX      hybrid; Influenza virus; non-structural protein 1; fusion.
XX
OS      Plasmodium falciparum.
OS      Influenza virus (A/PR/8/34).
XX
FH      Key
FH      Region
FT      1..81
FT      /label= N-terminal of NS1
FT      /note= "Influenza virus nonstructural protein 1"
XX
FT      Region
FT      82..97
FT      /label= immunodominant repeat region
FT      /note= "four variant tetrapeptide repeat units"
XX
FT      Peptide
FT      98..103
FT      /label= synthetic linker
FT      104
FT      /label= artifact
FT      /note= "see comments"
XX
FT      Region
FT      105..209
FT      /label= Aas 19-123 of CS protein
FT      /note= "Region I contg. flanking region less
XX      signal sequence"
FT      Region
FT      210
FT      /label= artifact
FT      /note= "see comments"
XX
FT      Region
FT      211..335
FT      /label= Aas 288-412 of CS protein
FT      /note= "Region II flanking region"
XX
PN      EP432965-A.
PD      19-JUN-1991.
XX
PF      06-DEC-1990; 90EP-0313257.
XX
PR      08-DEC-1989; 89US-0447746.
XX
PA      (SMIK ) SMITHKLINE BEECHAM.
PA      (USSA ) US SEC OF THE ARMY.
PA      (BIOM-) BIOMEDICAL RES INST.
XX
PI      Gross MS, Gordon DM, Hollingdale MR.
XX      WPI: 1991-179771/25.
DR
XX
PT      Polyptide comprising immunogenic determinants from P falciparum
PT      - for vaccine against malaria infection in humans.
XX
PS      Example 5; Page 11; 18pp; English.
XX
CC      The polyptide is prepd. by genetic engineering of genes encoding
CC      the P. falciparum circumsporozoite (CS) protein [Dame et al.,
CC      Science 225 : 593 (1984)], and the influenza virus non-structural
CC      protein 1 (NS1), [Baez et al., Nucleic Acids Research. 8 : 5645
CC      (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NS1
CC      (NS1_81) is linked to a synthetic sequence encoding four repeat
CC      units (the variant form) from the immunodominant region, which in
CC      turn is linked via a synthetic sequence to DNA encoding Region I

```

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CC      contg. flanking region less the 18 AA signal region. This is
CC      linked to DNA encoding Region II-contg. flanking region. The pro
CC      residue separating the Asp (at the C-terminal of the linker) from
CC      the Region I-contg. CS flanking region is an artifact of a filled-
CC      in BamHI site; the Gly separating the Region I and II-contg. CS
CC      flanking regions is an artifact of a synthetic FokI/TthIII I
CC      linker. The peptide can be used in a vaccine for protection
CC      against malaria.
CC      See also AAR12306-R12311 and AAR13175-R13178.
XX
SQ      Sequence 335 AA:

Query Match 100.0%; Score 109; DB 12; Length 335;
Best Local Similarity 100.0%; Pred. No. 7.7e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 DIEKICKMEKCSSVFNVNS 21
        ||||||||||||||||
DB      301 diekickmekcssvfnvns 321

RESULT  8
AAY70278
ID      AAY70278 standard; Protein: 350 AA.
XX
AC      AAY70278;
XX
DT      06-JUN-2000 (first entry)
XX
DE      Recombinant vaccine CDC/NIIMALVAC-1.
XX
KM      Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine;
KM      T-cell epitope; tetanus toxoid; antigenic epitope; treatment;
KM      circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2;
KM      liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2;
KM      apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175;
KM      EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen;
KM      Pfgr2; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody;
KM      honey bee.
XX
OS      Chimeric - Apis sp.
OS      Chimeric - Clostridium tetani.
OS      Chimeric - Plasmodium falciparum.
XX
FH      Key
FH      Peptide
FT      1..22
FT      /label= Melittin_signal_peptide
FT      /note= "Derived from Honey Bee"
XX
FT      Protein
FT      23..350
FT      /label= Mature_CDC/NIIMALVAC-1
FT      /note= "Recombinant multivalent malarial vaccine"
XX
PN      WO200011179-A1.
PD      02-MAR-2000.
XX
PF      19-AUG-1999; 99WO-US18869.
XX
PR      21-AUG-1998; 98US-0097703.
XX
PA      (NATIM-) NAT INST. IMMUNOLOGY.
PA      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI      Lal AA, Shi YP, Hasnain SE;
XX      WPI: 2000-237654/20.
DR      N-PsDB; AA251336.
XX
PT      Novel recombinant protein as vaccine for treating malarial infection
PT      comprises antigenic peptides obtained from different stages of
PT      plasmodium falciparum life cycle
XX

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PS Claim 3; Page 43-44; 52pp; English.  
 XX The present sequence is that of recombinant protein CDC/NIIMALVAC-1,  
 CC which is a multivalent, multistage malarial vaccine. The recombinant  
 CC protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope  
 CC from tetanus toxoid and 21 antigenic epitopes from circumsporozoite  
 CC protein (CSP), sporozoite surface protein-1 (MSP-1), MSP-2, apical  
 CC antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical  
 CC membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175),  
 CC thymoprotein-1 (TSP-1), and gamete specific antigen, Pf27.  
 CC These epitopes were obtained at different stages of the life cycle of  
 CC Plasmodium falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic  
 CC activity and can be used for treatment and prevention of malarial  
 CC infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting  
 CC P. falciparum in biological samples.  
 CC  
 SO Sequence 350 AA:

Query Match 100.0%; Score 109; DB 21; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 8,1e-09;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIEKICKMEKSSVFNVNS 21  
 ||||||||||||||||  
 DB 61 diekikmekssvfnyvns 81

RESULT 9  
 AAP83144  
 ID AAP83144 standard; protein; 411 AA.

XX AAP83144;  
 XX 20-NOV-1990 (first entry)  
 XX  
 XX Sequence encoded by the circumsporozoite (CS) gene from  
 DE Plasmodium falciparum.  
 XX  
 XX Vaccine; antigen; immunogen; probe; hybridisation;  
 KW immunosassay; diagnosis.  
 XX  
 XX Plasmodium falciparum.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH 106..120  
 FT Region /note="Region 1"  
 FT 147..206  
 FT Region /note="Repeat region, repeat unit = NANP"  
 FT 123..146  
 FT Region /note="Repeat region, repeat unit = NANPNDP"  
 FT 211..286  
 FT Region /note="Repeat region, repeat unit = NANP"  
 XX  
 XX EP278940-A.  
 PN  
 XX 17-AUG-1988.  
 PD  
 XX 25-JAN-1988; 88BP-0870008.  
 PE  
 XX 30-JAN-1987; 87US-0009325.  
 PR  
 XX (SMIK ) SMITH KLINE-RIT.  
 PA  
 XX Cabezon T, De Wilde M, Harford N;  
 PI  
 XX WPI: 1988-229751/33.  
 DR  
 DR N-PSDB; AAN81108.  
 XX  
 XX DNA encoding hepatitis B virus antigens and hybrids contg. them  
 PT used for expression in yeast to obtain vaccines and bivalent  
 PT vaccines  
 XX

PS Example; Fig 3Aa-3Af; 101pp; English.

XX Sequence of the CS gene (AAN81108) is from lambda-mpf1. A recombinant  
 CC DNA molecule is claimed, comprising functional DNA coding sequence fused,  
 CC in phase, to a portion of the Pre-S2 region of a hepatitis B virus (HBV)  
 CC Pre-S2-S protein coding sequence. The functional DNA coding sequence of  
 CC comprises the Pre-S2 coding sequence, the CS protein coding sequence of  
 CC Pre-S1-Pre-S2 coding sequence, the CS protein coding sequence of  
 CC Plasmodium, or a HIV coding sequence such as  
 CC an HIV envelope gene sequence, e.g. HIV C7 protein coding region, HIV  
 CC Peptide 121 coding region, or HIV Dressman peptide coding region.  
 CC  
 SO Sequence 411 AA:

Query Match 100.0%; Score 109; DB 9; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 9,6e-09;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIEKICKMEKSSVFNVNS 21  
 ||||||||||||||||  
 DB 377 diekikmekssvfnyvns 397

RESULT 10  
 AAP60416  
 ID AAP60416 standard; protein; 412 AA.

XX AAP60416;  
 XX 13-JUN-1991 (first entry)  
 XX  
 XX CS protein of malaria parasite.  
 DE  
 XX Sporozoite; vaccination.  
 KW  
 XX Plasmodium falciparum.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH 124..127  
 FT Region /label= Repeat unit  
 FT  
 XX  
 XX EPI6410-A.  
 PN  
 XX 02-JAN-1986.  
 PD  
 XX 24-JUN-1985; 85EP-0107794.  
 PE  
 XX 26-JUN-1984; 84US-0624564.  
 PR  
 XX (USDC ) US SEC OF COMMERCE.  
 PA (USGO ) US GOVERNMENT.  
 PA (USSA ) US SEC OF THE ARMY.  
 XX  
 XX McCutchan TF, Dame JB, Williams JL, Schneider I;  
 PI  
 XX WPI: 1986-008635/02.  
 DR N-PSDB; AAN60362.  
 DR  
 XX New immunologically active pure synthetic peptide(s) - used for  
 PT protection against infection by malaria parasite.  
 PT  
 XX Disclosure; Fig 2; 49pp; English.  
 PS  
 XX The Plasmodium CS gene was used to isolate peptides capable of  
 CC inducing an immune response to the parasite. Peptide antigens may  
 CC be synthesised in pure form and used to generate an immune  
 CC response in vaccination against malaria. The featured repeat  
 CC units are claimed and must be present in copies of 2-1000.  
 CC  
 SO Sequence 412 AA:



Query Match 100.0%; Score 109; DB 7; Length 412;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-09;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIEKICKMEKCSVFNVNS 21  
 ||||||||||||||||||  
 DB 378 diekikmekcsvfnnvns 398

## RESULT 11

AAR37796  
 ID AAR37796 standard; Protein: 424 AA.

AC AAR37796;

DT 27-SEP-1993 (first entry)

DE RTS protein.

KW RTS: expression cassette: hybrid protein: S. cerevisiae; TDH3;  
 cloning; circumsporozoite protein; CSP; Plasmodium falciparum;  
 strain 7G8; hepatitis B virus; HBV; adw serotype; pres2 protein;

KM S protein.

OS Synthetic.

XX Location/Qualifiers

FT 1 /note= "Derived from S. cerevisiae TDH3 gene sequence"

FT 2..4 /note= "Cloning artefact"

FT 5..193 /note= "Represents amino acids 210-398 of the CSP of  
 P. falciparum"

FT 194..197 /note= "Carboxy terminal amino acids from HBV (adw  
 serotype) pres2 protein"

FT Protein /note= "S protein of HBV (adw serotype)"

FT MO9310152-A.

XX 27-MAY-1993.

PD 11-NOV-1992; 92WO-EP02591.

PE 16-NOV-1991; 91GB-0024390.

PR 27-FEB-1992; 92US-0842694.

XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

PA Cohen J, De Wilde M;

PI WPI: 1993-182494/22.

DR N-PSDB; AAO42566.

XX Hybrid protein comprising Plasmodium circumsporozoite protein and  
 PT HBsAg - useful as a vaccine for treating patients susceptible to  
 PT Plasmodium infections

XX Disclosure: Fig 5; 59pp; English.

PS This sequence represents the RTS hybrid protein which is encoded by  
 CC the RTS expression cassette. This hybrid consists of a methionine  
 CC residue derived from S. cerevisiae TDH3 gene sequence, three amino  
 CC acids, Met-Ala-Pro, derived from a nucleotide sequence created by  
 CC the cloning procedure used to construct the hybrid gene, a stretch  
 CC of 189 amino acids representing amino acids 210 to 398 of the  
 CC circumsporozoite protein (CSP) of Plasmodium falciparum strain 7G8,  
 CC an amino acid Arg created by the cloning procedure, four amino acids,  
 CC Pro-Val-Thr-Asn, representing the four carboxy terminal residues of  
 CC hepatitis B virus (HBV), adw serotype, pres2 protein, and a stretch  
 CC of 226 amino acids specifying the S protein of HBV, adw serotype.

CC This protein, and RTS\* (see also AAR37797), may be combined with an  
 CC adjuvant and used in a vaccine for preventing plasmodium infections.  
 CC The vaccines produce a humoral response and also a cellular immune  
 CC response.

XX Sequence 424 AA;

Query Match 100.0%; Score 109; DB 14; Length 424;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-09;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIEKICKMEKCSVFNVNS 21  
 ||||||||||||||||||  
 DB 173 diekikmekcsvfnnvns 193

## RESULT 12

AAR37797  
 ID AAR37797 standard; Protein: 424 AA.

AC AAR37797;

DT 27-SEP-1993 (first entry)

DE RTS\* protein.

KW RTS: expression cassette: hybrid protein: S. cerevisiae; TDH3;  
 cloning; circumsporozoite protein; CSP; Plasmodium falciparum;  
 strain 7G8; hepatitis B virus; HBV; adw serotype; pres2 protein;

KM S protein.

XX Synthetic.

XX Location/Qualifiers

FT 1 /note= "Derived from S. cerevisiae TDH3 gene sequence"

FT 2..4 /note= "Cloning artefact"

FT 5..193 /note= "Represents amino acids 210-398 of the CSP of  
 P. falciparum"

FT 194..197 /note= "Carboxy terminal amino acids from HBV (adw  
 serotype) pres2 protein"

FT Protein /note= "S protein of HBV (adw serotype)"

FT MO9310152-A.

XX 27-MAY-1993.

PD 11-NOV-1992; 92WO-EP02591.

PE 16-NOV-1991; 91GB-0024390.

PR 27-FEB-1992; 92US-0842694.

XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

PA Cohen J, De Wilde M;

PI WPI: 1993-182494/22.

DR N-PSDB; AAO42567.

XX Hybrid protein comprising Plasmodium circumsporozoite protein and  
 PT HBsAg - useful as a vaccine for treating patients susceptible to  
 PT Plasmodium infections

XX Disclosure: Fig 9; 59pp; English.

PS This sequence represents the RTS\* hybrid protein which is encoded by  
 CC the RTS\* expression cassette. This hybrid consists of a methionine  
 CC residue derived from S. cerevisiae TDH3 gene sequence, three amino

CC Plasmid WR201 was obtained from the Walter Reed Army Institute of  
CC Research, and results from insertion of a 2.3 kb EcoRI fragment from

CC peptide CS.73 (residues 1-21) corresponds to residues 378-398 of the  
CC protein from *P. falciparum* but contains 2 Ala residues in place

CC of the native protein's Cys residues at positions 384 and 389. Also  
 CC claimed is AAP91504 (or modified forms, see PT) associated with an  
 CC antigenic structure representing a B-cell epitope, pref. a multiple  
 CC antigenic peptide, esp. multimers of the repeat sequences NAMP  
 CC present in P. falciparum CS protein.  
 XX  
 SQ Sequence 21 AA:

Query Match 83.5%; Score 91; DB 10; Length 21;  
 Best Local Similarity 90.5%; Pred. No. 2.4e-07;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIEKKICKMEKCSYFNVNVS 21  
 ||||| |||| |||||  
 Db 1 diekkickmekassvfnvns 21

RESULT 15

AAR82586  
 ID AAR82586 standard; peptide: 21 AA.

XX  
 AC AAR82586;

XX 13-JUN-1996 (first entry)

XX Plasmodium falciparum circumsporozoite helper T cell epitope, PF.

XX IGE; CH4; Immunoglobulin; epsilon; Immunogen; helper T cell; epitope;  
 KW vaccine; allergy; antibody; constant heavy chain.

XX Plasmodium falciparum.

XX W09526365-A1.

XX 05-OCT-1995.

XX 24-MAR-1995; 95WO-US03741.

XX 25-OCT-1994; 94US-0328912.

XX 28-MAR-1994; 94US-0218461.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

XX WPI; 1995-351297/45.

XX Synthetic peptide-based immunogen contg. IGE CH4 peptide and helper  
 PT T cell epitope - useful for eliciting antibody prodn. for allergy  
 PT treatment

XX Claim 3; Page 23; 87pp; English.

XX AAR82571-91 are helper T cell epitopes which can be used in the  
 CC preparation of a peptide immunogen that is useful in vaccines for  
 CC treating allergic reactions. In the immunogen an IGE CH4 peptide  
 CC is attached C-terminally to a series of amino acids including a  
 CC helper T cell epitope. The immunogen may also opt. contain a fatty  
 CC acid or fatty acid derivative, an invasins domain or alpha-NH2. The  
 CC immunogen produces high titres of antibodies to the effector site  
 CC in human IGE heavy chain (the CH4 domain peptide) which inhibit mast  
 CC cell activation and reduce allergen-induced IGE prodn. The immunogens  
 CC may be used in either a radially branching multimeric form or a  
 CC linearly arranged monomeric form.

XX Sequence 21 AA:

Query Match 83.5%; Score 91; DB 16; Length 21;  
 Best Local Similarity 90.5%; Pred. No. 2.4e-07;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIEKKICKMEKCSYFNVNVS 21  
 ||||| |||| |||||  
 Db 1 diekkickmekassvfnvns 21

Search completed: January 29, 2002, 10:21:43  
 Job time: 419 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using SW model

Run on: January 29, 2002, 10:24:03 ; Search time 133.18 Seconds  
(without alignments)  
3.548 Million cell updates/sec

Title: US-09-763-397A-7

Perfect score: 109

Sequence: 1 DIEKICKMEKSSVFNVNVS 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	100.0	412	1	US-08-313-288B-18
2	109	100.0	423	2	US-08-760-797A-1
3	109	100.0	424	2	US-08-760-797A-3
4	109	100.0	424	4	US-08-932-929B-1
5	109	100.0	424	4	US-08-932-929B-3
6	91	83.5	21	1	US-08-186-266-6
7	91	83.5	21	1	US-08-446-692-48
8	91	83.5	21	2	US-08-446-692-48
9	91	83.5	21	2	US-08-488-351A-48
10	91	83.5	21	5	US-09-100-409A-54
11	91	83.5	21	5	PCR-US95-02121-97
12	91	83.5	21	5	PCR-US95-13841-20
13	91	83.5	33	1	US-08-446-692-27
14	83	76.1	478	3	US-08-488-351A-27
15	75.5	69.3	20	1	US-08-155-888-2
16	75.5	69.3	20	5	US-08-465-167A-20
17	71	65.1	15	2	PCR-US92-07218-17
18	71	65.1	17	5	US-08-318-856A-75
19	71	65.1	17	5	PCR-US95-02121-96
20	71	65.1	66	2	US-08-455-625-35
21	71	65.1	66	4	US-08-455-685-35
22	71	65.1	66	4	US-08-060-988A-35
23	69	63.3	378	6	PCR-US94-05142-35
24	67	61.5	15	6	5171843-9
25	62	56.9	15	6	US-08-817-933A-7
26	61	56.0	21	1	5169933-30
27	55.5	50.9	16	1	US-08-305-871A-12
					Sequence 19, Appl

28	55.5	50.9	16	5	PCR-US92-07218-16	Sequence 16, Appl
29	48	44.0	15	2	US-08-318-856A-76	Sequence 76, Appl
30	47	43.1	492	4	US-08-845-258-21	Sequence 21, Appl
31	47	43.1	492	4	US-08-990-571-21	Sequence 21, Appl
32	47	43.1	492	4	US-08-723-142A-21	Sequence 21, Appl
33	47	43.1	503	4	US-08-845-258-52	Sequence 52, Appl
34	47	43.1	503	4	US-08-990-571-52	Sequence 52, Appl
35	46	42.2	1400	1	US-08-080-255-7	Sequence 7, Appl
36	46	42.2	1400	3	US-08-465-713-7	Sequence 7, Appl
37	46	42.2	1400	5	PCR-US93-05857-7	Sequence 7, Appl
38	46	42.2	3969	4	US-08-061-376-5	Sequence 5, Appl
39	39.5	36.2	159	6	5208144-35	Patent No. 5208144
40	39	35.8	77	2	US-08-465-380-58	Sequence 58, Appl
41	39	35.8	77	2	US-08-486-397-58	Sequence 58, Appl
42	39	35.8	77	2	US-08-486-399-58	Sequence 58, Appl
43	39	35.8	77	2	US-08-461-965-58	Sequence 58, Appl
44	39	35.8	77	2	US-08-634-641-58	Sequence 58, Appl
45	39	35.8	77	2	US-09-249-471-58	Sequence 58, Appl

## ALIGNMENTS

RESULT 1  
US-08-313-288B-18  
Sequence 18, Application US/08313288B  
Patent No. 5750502  
GENERAL INFORMATION:  
APPLICANT: Jessell, Thomas M. and Avihu Klar  
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/313,288B  
FILING DATE: January 5, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0526  
TELEX:  
INFORMATION FOR SEQ. ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 412 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-313-288B-18  
Query Match 100.0%; Score 109; DB 1; Length 412;  
Best Local Similarity 100.0%; Pred. No. 8.4e-09;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 DIEKICKMEKSSVFNVNVS 21  
DB 378 DIEKICKMEKSSVFNVNVS 398

RESULT 2  
US-08-760-797A-1  
; Sequence 1, Application US/08760797A  
; Patent No. 5928902  
; GENERAL INFORMATION:  
; APPLICANT: De Wilde, Michel  
; APPLICANT: Cohen, Joseph  
; TITLE OF INVENTION: Hybrid Protein Between CS  
; TITLE OF INVENTION: From Plasmodium and HBSAG  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/760,797A  
; FILING DATE: 04-DEC-1996  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/442,612  
; FILING DATE: 17-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baumeister, Kirk  
; REGISTRATION NUMBER: 33,833  
; REFERENCE/DOCKET NUMBER: B45015-1C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5096  
; TELEFAX: 610-270-5090  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 423 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-760-797A-1

Query Match 100.0%; Score 109; DB 2; Length 423;  
Best Local Similarity 100.0%; Pred. No. 8,6e-09;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIEKICKMEKCSVFNVNS 21  
|||||  
DB 172 DIEKICKMEKCSVFNVNS 192

RESULT 3  
US-08-760-797A-3  
; Sequence 3, Application US/08760797A  
; Patent No. 5928902  
; GENERAL INFORMATION:  
; APPLICANT: De Wilde, Michel  
; APPLICANT: Cohen, Joseph  
; TITLE OF INVENTION: Hybrid Protein Between CS  
; TITLE OF INVENTION: From Plasmodium and HBSAG  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA

ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/760,797A  
; FILING DATE: 04-DEC-1996  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/442,612  
; FILING DATE: 17-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baumeister, Kirk  
; REGISTRATION NUMBER: 33,833  
; REFERENCE/DOCKET NUMBER: B45015-1C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5096  
; TELEFAX: 610-270-5090  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 424 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-760-797A-3

Query Match 100.0%; Score 109; DB 2; Length 424;  
Best Local Similarity 100.0%; Pred. No. 8,7e-09;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIEKICKMEKCSVFNVNS 21  
|||||  
DB 169 DIEKICKMEKCSVFNVNS 189

RESULT 4  
US-08-932-929B-1  
; Sequence 1, Application US/08932929B  
; Patent No. 6169171  
; GENERAL INFORMATION:  
; APPLICANT: De Wilde, Michel  
; APPLICANT: Cohen, Joseph  
; TITLE OF INVENTION: Hybrid Protein Between CS  
; TITLE OF INVENTION: From Plasmodium and HBSAG  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/932,929B  
; FILING DATE:  
; CLASSIFICATION:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/760,797  
; FILING DATE: 04-DEC-1996  
; APPLICATION NUMBER: 08/442,612  
; FILING DATE: 17-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baumeister, Kirk  
; REGISTRATION NUMBER: 33,833

```

; REFERENCE/DOCKET NUMBER: B45015-1FWC2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-932-9298-1

Query Match      100.0%; Score 109; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIEKKICKMEKSSVFNVNYS 21
   ||||||||||||||||
Db 173 DIEKKICKMEKSSVFNVNYS 193

RESULT 5
US-08-932-9298-3
; Sequence 3, Application US/08932929B
; Patent No. 6169171
;
; GENERAL INFORMATION:
; APPLICANT: De Wilde, Michel
; APPLICANT: Cohen, Joseph
; TITLE OF INVENTION: Hybrid Protein Between CS
; TITLE OF INVENTION: from Plasmodium and HbA2G
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/932,929B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,797
; FILING DATE: 04-DEC-1996
; APPLICATION NUMBER: 08/442,612
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: B45015-1FWC2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
;
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-932-9298-3

Query Match      100.0%; Score 109; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
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```

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIEKKICKMEKSSVFNVNYS 21
   ||||||||||||||||
Db 169 DIEKKICKMEKSSVFNVNYS 189

RESULT 6
US-08-186-266-6
; Sequence 6, Application US/08186266
; Patent No. 5662907
;
; GENERAL INFORMATION:
; APPLICANT: KUBO, Ralph T.
; APPLICANT: GREY, Howard M.
; APPLICANT: SETTE, Alessandro
; APPLICANT: CELIS, Esteban
; TITLE OF INVENTION: INDUCTION OF ANTI-TUMOR CYTOTOXIC
; TITLE OF INVENTION: T LYMPHOCYTES IN HUMANS USING
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,266
; FILING DATE: 25-JAN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/159,339
; FILING DATE: 29-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-50-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..21
; OTHER INFORMATION: /note="Plasmodium falciparum CS
; OTHER INFORMATION: protein at positions 378-398."
;
US-08-186-266-6

Query Match      83.5%; Score 91; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 2.1e-07;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
Qy 1 DIEKICKMEKCSSVFNVNS 21
    ||||| |||| ||||| ||||
Db 1 DIEKIATMEKASSVFNVNS 21
```

RESULT 7  
 US-08-446-692-48  
 : Sequence 48, Application US/08446692  
 : Patent No. 5759551  
 :  
 : GENERAL INFORMATION:  
 : APPLICANT: Ladd, Anna  
 : APPLICANT: Wang, Chang yi  
 : TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
 : TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines  
 : NUMBER OF SEQUENCES: 114  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Maria C.H. Lin  
 : STREET: 345 Park Avenue  
 : CITY: New York  
 : STATE: NY  
 : COUNTRY: US  
 : ZIP: 10154-0053  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patentin Release #1.0, Version #1.25  
 :  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/446,692  
 : FILING DATE: 7-JUN-1995  
 : CLASSIFICATION: 424  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Maria C.H. Lin  
 : REGISTRATION NUMBER: 29,323  
 : REFERENCE/DOCKET NUMBER: 1151-4146 US2  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (212)415-8745  
 : TELEFAX: (516)751-6849  
 : INFORMATION FOR SEQ ID NO: 48:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 21 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 :  
 : MOLECULE TYPE: peptide  
 :  
 : US-08-446-692-48

```

Query Match      83.5%; Score 91; DB 1; Length 21;
Best Local Similarly 90.5%; Pred. No. 2.1e-07;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1 DIEKICKMEKCSVFNVNVS 21
        ||||| ||| |||||
Db      1 DIEKIKAMEKASSVFNVNS 21

RESULT      8
US-08-488-351A-48
; Sequence 48; Application US/08488351A
; Patent No. 5643446
;
; GENERAL INFORMATION:
;
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang YI
; APPLICANT: Zamb, Timothy
;
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; and synthetic universal immune stimulants for vaccines
;
; NUMBER OF SEQUENCES: 114
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
;
;
;

```

COUNTRY: US  
ZIP: 10154-0053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,351A  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/446,692  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/229,275  
FILING DATE: 14-APR-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,166  
FILING DATE: 27-APR-1992  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maria C.H. Lin  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 1151-4146 US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)415-8745  
TELEFAX: (516)751-6649  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-488-351A-48

```

Query Match      83.5%;   Score 91;   DB 2;   Length 21;
Best Local Similarity 90.5%;   Pred. No. 2.1e-07;
Matches 19;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

OY      1   DIEKICKMEKCSVFENVVNS 21
        ||||| ||||| ||||| |||
DB      1   DIEKIAKMEKASVFENVVNS 21

RESULT 9
US-09-100-409A-54
; Sequence 54, Application US/09100409A
; Patent No. 6090388
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang YI
; TITLE OF INVENTION: PEPTIDE COMPOSITION FOR
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF HIV INFECTION AND
; TITLE OF INVENTION: IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patentin Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100.409A
;

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FILED DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME:  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 1151-4154  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-100-409A-54

Query Match 83.5%; Score 91; DB 3; Length 21;  
Best Local Similarity 90.5%; Pred. No. 2.1e-07;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIEKICKMEKSSVFNVVNS 21  
||||| ||||| ||||| ||||| |||||  
DB 1 DIEKIKAKMEKASSVFNVVNS 21

RESULT 10  
PCT-US95-02121-97  
Sequence 97, Application PC/TUS9502121  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
TITLE OF INVENTION: CTL IMMUNITY  
NUMBER OF SEQUENCES: 153  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/02121  
FILING DATE: 16-FEB-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/197,484  
FILING DATE: 16-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/935,811  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/874,491  
FILING DATE: 27-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,682  
FILING DATE: 29-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/749,568  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 14137-26-4PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 467-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 97:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide

FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..21  
OTHER INFORMATION: /note="Malaria circumsporozoite"  
OTHER INFORMATION: 378-398"  
PCT-US95-02121-97

Query Match 83.5%; Score 91; DB 5; Length 21;  
Best Local Similarity 90.5%; Pred. No. 2.1e-07;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIEKICKMEKSSVFNVVNS 21  
||||| ||||| ||||| ||||| |||||  
DB 1 DIEKIKAKMEKASSVFNVVNS 21

RESULT 11  
PCT-US95-13841-20  
Sequence 20, Application PC/TUS9513841  
GENERAL INFORMATION:  
APPLICANT: United Biomedical Inc; Walfield, Alan M.;  
APPLICANT: Wang, Chang Yi  
TITLE OF INVENTION: Synthetic Ige Membrane Anchor  
TITLE OF INVENTION: Peptide Immunogens for the Treatment of Allergy  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Maria C.H. Lin  
STREET: 345 Park Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13841  
FILING DATE: 25-OCT-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/328,519  
FILING DATE: 25-OCT-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lin, Maria C.H.  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 1151-4117  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US95-13841-20

Query Match 83.5%; Score 91; DB 5; Length 21;  
Best Local Similarity 90.5%; Pred. No. 2.1e-07;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIEKICKMEKSSVFNVVNS 21  
||||| ||||| ||||| ||||| |||||  
DB 1 DIEKIKAKMEKASSVFNVVNS 21

RESULT 12

US-08-446-692-27  
Sequence 27, Application US/08446692  
Patent No. 5759551  
GENERAL INFORMATION:  
APPLICANT: Ladd, Anna  
APPLICANT: Wang, Chang Yi  
APPLICANT: Zamb, Timothy  
TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
TITLE OF INVENTION: and synthetic universal immune stimulants for vaccines  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Maria C.H. Lin  
STREET: 345 Park Avenue  
CITY: New York  
STATE: NY  
COUNTRY: US  
ZIP: 10154-0053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,692  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maria C.H. Lin  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 1151-4146 US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)415-8745  
TELEFAX: (516)751-6849  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-446-692-27

Query Match 83.5%; Score 91; DB 1; Length 33;  
Best Local Similarity 90.5%; Pred. No. 3.3e-07;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIEKIKMEKCSVFNVNS 21  
DB 1 DIEKIKMEKCSVFNVNS 21

RESULT 13  
US-08-488-351A-27  
Sequence 27, Application US/08488351A  
Patent No. 5843446  
GENERAL INFORMATION:  
APPLICANT: Ladd, Anna  
APPLICANT: Wang, Chang Yi  
APPLICANT: Zamb, Timothy  
TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
TITLE OF INVENTION: and synthetic universal immune stimulants for vaccines  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Maria C.H. Lin  
STREET: 345 Park Avenue  
CITY: New York  
STATE: NY  
COUNTRY: US  
ZIP: 10154-0053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,351A  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/446,692  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/229,275  
FILING DATE: 14-APR-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,166  
FILING DATE: 27-APR-1992  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maria C.H. Lin  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 1151-4146 US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)415-8745  
TELEFAX: (516)751-6849  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-488-351A-27

Query Match 83.5%; Score 91; DB 2; Length 33;  
Best Local Similarity 90.5%; Pred. No. 3.3e-07;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIEKIKMEKCSVFNVNS 21  
DB 1 DIEKIKMEKCSVFNVNS 21

RESULT 14  
US-08-155-888-2  
Sequence 2, Application US/08155888  
Patent No. 6066623  
GENERAL INFORMATION:  
APPLICANT: Hoffman, Stephen J.  
APPLICANT: Hedstrom, Richard C.  
APPLICANT: Sedegah, Martha  
TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE PROTECTIVE  
TITLE OF INVENTION: AGAINST MALARIA, METHODS OF PROTECTION AND VECTOR FOR  
DELIVERING POLYNUCLEOTIDE VACCINES  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Naval Medical Res. & Dev. Cnd.  
STREET: Bldg. 1, T-12 8901 Wisconsin Ave.  
CITY: Bethesda  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20889-5606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/155,888  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Spevack, A. David  
REGISTRATION NUMBER: 24,743

REFERENCE/DOCKET NUMBER: N.C. 75,851  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 295-6759  
TELEFAX: (202) 295-1022  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 478 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-155-888-2

Query Match 76.1%; Score 83; DB 3; Length 478;  
Best Local Similarity 61.9%; Pred. No. 6.6e-05;  
Matches 13; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

OY 1 DIEKKICKMEKCSYFNVVNS 21  
||:|||||:|:|:  
Db 444 DIDFKKMKCSIFNIVSN 464

RESULT 15  
US-08-465-167A-20  
Sequence 20, Application US/08465167A  
Patent No. 5750395  
GENERAL INFORMATION:  
APPLICANT: Fikes, John D.  
APPLICANT: Livingston, Brian D.  
APPLICANT: Sette, Alessandro D.  
APPLICANT: Sidney, John C.  
TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL  
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 96111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,167A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/103,623  
FILING DATE: 06-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 14137-60-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRADEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-465-167A-20

Query Match 69.3%; Score 75.5; DB 1; Length 20;  
Best Local Similarity 85.7%; Pred. No. 3.9e-05;  
Matches 18; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 1 DIEKKICKMEKCSYFNVVNS 21  
||||| | | ||||| |  
Db 1 DIEKKIKMK-KASSYFNVVNS 20

Search completed: January 29, 2002, 10:24:03  
Job time: 509 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 10:26:36 ; Search time 144.96 Seconds  
(without alignments)

11.035 Million cell updates/sec

Title: US-09-763-397a-7

Perfect score: 109

Sequence: 1 DIEKICKMEKSSVFNVNS 21

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	100.0	405	2 S05428	circumsporozoite p
2	109	100.0	412	1 OZ2QAF	circumsporozoite p
3	109	100.0	424	2 A54533	circumsporozoite p
4	109	100.0	442	2 A54529	circumsporozoite p
5	107	98.2	388	2 A39756	circumsporozoite p
6	83	76.1	264	2 A44969	circumsporozoite p
7	83	76.1	332	1 OZ2OMB	circumsporozoite p
8	83	76.1	348	1 OZ2OBK	circumsporozoite p
9	83	76.1	367	1 OZ2OMY	circumsporozoite p
10	77	70.6	429	2 A54504	circumsporozoite p
11	77	70.6	485	2 A60610	circumsporozoite p
12	71	65.1	378	1 OZ2OAB	circumsporozoite p
13	71	65.1	378	1 OZ2OAL	circumsporozoite p
14	71	65.1	398	1 OZ2OAS	circumsporozoite p
15	71	65.1	401	1 OZ2OAC	circumsporozoite p
16	71	65.1	419	1 OZ2OAM	circumsporozoite p
17	70.5	64.7	388	2 JG6164	circumsporozoite p
18	69	63.3	343	2 A29319	circumsporozoite p
19	69	63.3	367	2 A32068	circumsporozoite p
20	69	63.3	378	1 OZ2OAV	circumsporozoite p
21	69	63.3	386	2 A48571	circumsporozoite p
22	69	63.3	387	2 D41156	circumsporozoite p
23	69	63.3	387	2 C41156	circumsporozoite p
24	69	63.3	395	2 A41156	circumsporozoite p
25	65	59.6	351	1 OZ2OKU	circumsporozoite p
26	65	59.6	363	1 OZ2OKA	circumsporozoite p
27	51	46.8	636	2 A86248	protein T23J18.9 l
28	51	46.8	926	2 T15683	hypothetical prote
29	46	42.2	191	2 S70284	outer surface prote

30	46	42.2	480	2 T20168	hypothetical prote
31	46	42.2	1282	2 JE0120	glycoprotein A - m
32	46	42.2	3869	2 A48205	All-1 protein +GRE
33	46	42.2	3968	2 A44265	trichorax homolog
34	45	41.3	274	2 S59785	probable membrane
35	45	41.3	298	2 A70238	hypothetical prote
36	44	40.4	327	1 RDVZAS	ribonucleoside-dip
37	44	40.4	379	2 B64473	hypothetical prote
38	44	40.4	715	2 JC2222	major surface glyc
39	44	40.4	763	2 T22843	hypothetical prote
40	44	40.4	803	2 S26823	zinc finger protei
41	44	40.4	957	2 T15976	hypothetical prote
42	44	40.4	2339	2 A45597	DNA-directed RNA p
43	43.5	39.9	280	2 S47815	hypothetical 31.8k
44	43.5	39.9	280	2 F86034	hypothetical prote
45	43	39.4	117	2 T07645	PEARL I protein h

#### ALIGNMENTS

RESULT 1  
S05428  
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate NF54)  
C:Species: Plasmodium falciparum  
C:Date: 07-Jun-1990 #sequence: revision 07-Jun-1990 #text\_change 09-Jun-2000  
C:Accession: S05428; A45527; I60657  
R:Campbell, J.R.  
Nucleic Acids Res. 17, 5854, 1989  
A:Title: DNA sequence of the gene encoding a Plasmodium falciparum malaria candidate  
A:Reference number: S05428; MUID:89345189  
A:Accession: S05428  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-405 <CAM>  
A:Cross-references: EMBL:X15363  
R:Caspers, P.; Gentz, R.; Matile, H.; Pink, J.R.; Sinigaglia, F.  
Mol. Biochem. Parasitol. 35, 185-190, 1989  
A:Title: The circumsporozoite protein gene from NF54, a Plasmodium falciparum isolate  
A:Reference number: A45527; MUID:89364958  
A:Accession: A45527  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-405 <CAS>  
A:Cross-references: GB:M22982; GB:J04650; NID:9160168; PIDN:AAA29527.1; PID:9160169  
R:Lockyer, M.C.; Marsh, K.; Newbold, C.L.  
Mol. Biochem. Parasitol. 37, 275-280, 1989  
A:Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell  
A:Reference number: A60657; MUID:90114334  
A:Accession: I60657  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 319-336, 354-373 <LOC>  
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology  
F:J29-383/Domain: thrombospondin type 1 repeat homology <TNRI>

Query Match 100.0%; Score 109; DB 2; Length 405;  
Best Local Similarity 100.0%; Pred. No. 1.5e-08;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIEKICKMEKSSVFNVNS 21  
DB 371 DIEKICKMEKSSVFNVNS 391

RESULT 2  
OZ2QAF  
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate INTM22)  
C:Species: Plasmodium falciparum  
C:Date: 15-Nov-1984 #sequence\_revision 15-Nov-1984 #text\_change 09-Jun-2000  
C:Accession: A03388  
R:Name, J.B.; Williams, J.L.; McCutchan, T.F.; Weber, J.L.; Wirtz, R.A.; Hochmeyer, W

Science 225, 593-599, 1984  
A:Title: Structure of the gene encoding the immunodominant surface antigen on the sporozoite  
A:Reference number: A03388; MUID:84250215  
A:Accession: A03388  
A:Molecule type: DNA  
A:Residues: 1-412 <DAM>  
A:Cross-references: GB:K02194; NID:g160160; PIDN:AAA29524.1; PID:g160161  
A:Experimental source: clone 7c8  
C:Comment: Residues 1-16 are the probable signal sequence.  
C:Comment: There are 41 copies of a 4-residue repeating unit in the middle domain of the protein.  
F:336-390/Domain: thrombospondin type 1 repeat homology <THRI>

Query Match 100.0%; Score 109; DB 1; Length 412;  
Best Local Similarity 100.0%; Pred. No. 1.5e-08;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIEKICKMEKCSVFNNVNS 21  
|||||  
Db 378 DIEKICKMEKCSVFNNVNS 398

RESULT 3  
A:Accession: A54533  
A:Title: Circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain T4, Thailand)  
C:Species: Plasmodium falciparum  
C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jun-2000  
C:Accession: A54533  
R:Del Portillo, H.A.; Nussenzweig, R.S.; Enea, V.  
Mol. Biochem. Parasitol. 24, 289-294, 1987  
A:Title: Circumsporozoite gene of a Plasmodium falciparum strain from Thailand.  
A:Reference number: A54533; MUID:87315205  
A:Accession: A54533  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-424 <DEI>  
A:Cross-references: GB:M19752; NID:g160216; PIDN:AAA29555.1; PID:g160217  
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology  
F:348-402/Domain: thrombospondin type 1 repeat homology <THRI>

Query Match 100.0%; Score 109; DB 2; Length 424;  
Best Local Similarity 100.0%; Pred. No. 1.5e-08;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIEKICKMEKCSVFNNVNS 21  
|||||  
Db 390 DIEKICKMEKCSVFNNVNS 410

RESULT 4  
A:Accession: A54529  
A:Title: Circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain Wellcome)  
C:Species: Plasmodium falciparum  
C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jun-2000  
C:Accession: A54529  
R:Lockyer, M.J.; Schwarz, R.T.  
Mol. Biochem. Parasitol. 22, 101-108, 1987  
A:Title: Strain variation in the circumsporozoite protein gene of Plasmodium falciparum.  
A:Reference number: A54529; MUID:87115616  
A:Accession: A54529  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-442 <LOC>  
A:Cross-references: GB:M15505; NID:g160214; PIDN:AAA29554.1; PID:g160215  
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology  
C:Keywords: tandem repeat  
F:366-420/Domain: thrombospondin type 1 repeat homology <THRI>

Query Match 100.0%; Score 109; DB 2; Length 442;  
Best Local Similarity 100.0%; Pred. No. 1.6e-08;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIEKICKMEKCSVFNNVNS 21  
|||||  
Db 408 DIEKICKMEKCSVFNNVNS 428

RESULT 5  
A:Accession: A39756  
A:Title: Circumsporozoite protein - Plasmodium reichenowi  
C:Species: Plasmodium reichenowi  
C:Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 20-Aug-1999  
C:Accession: A39756  
R:Lal, A.A.; Goldman, I.F.  
J. Biol. Chem. 266, 6686-6689, 1991  
A:Title: Circumsporozoite protein gene from Plasmodium reichenowi, a chimpanzee malar  
A:Reference number: A39756; MUID:91201303  
A:Accession: A39756  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-388 <LAL>  
A:Cross-references: GB:M60972; NID:g160228; PIDN:AAA29561.1; PID:g160229  
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology  
F:312-366/Domain: thrombospondin type 1 repeat homology <THRI>

Query Match 98.2%; Score 107; DB 2; Length 388;  
Best Local Similarity 95.2%; Pred. No. 2.8e-08;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIEKICKMEKCSVFNNVNS 21  
|||||  
Db 354 DIEKICKMEKCSVFNNVNS 374

RESULT 6  
A:Accession: A44969  
A:Title: Circumsporozoite protein precursor - Plasmodium yoelii nigeriensis  
C:Species: Plasmodium yoelii nigeriensis  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 01-Dec-1995  
C:Accession: A44969  
R:Colomer-Gould, V.; Enea, V.  
Mol. Biochem. Parasitol. 43, 51-58, 1990  
A:Title: Plasmodium yoelii nigeriensis circumsporozoite gene structure and its implic  
A:Reference number: A44969; MUID:91148645  
A:Accession: A44969  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-264 <COL>  
A:Cross-references: GB:M32350  
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology  
F:190-242/Domain: thrombospondin type 1 repeat homology <THRI>

Query Match 76.1%; Score 83; DB 2; Length 264;  
Best Local Similarity 61.9%; Pred. No. 6.5e-05;  
Matches 13; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIEKICKMEKCSVFNNVNS 21  
||:|||||  
Db 230 DIDTEICKMKDCSIFNIVNS 250

RESULT 7  
A:Accession: OZQ0MB  
A:Title: Circumsporozoite protein precursor - Plasmodium berghei (strain NK65)  
N:Alternate names: sporozoite surface antigen  
C:Species: Plasmodium berghei  
C:Date: 30-Sep-1987 #sequence\_revision 28-Jul-1995 #text\_change 16-Jul-1999  
C:Accession: A44948; A25083; S13446  
R:Lanar, D.E.  
Mol. Biochem. Parasitol. 39, 151-154, 1990  
A:Title: Sequence of the circumsporozoite gene of Plasmodium berghei ANKA clone and N

A:Reference number: A44948; MUID:90158693  
A:Accession: A44948  
A:Molecule type: DNA  
A:Residues: 1-332 <LAN>  
A:Cross-references: GB:M28887  
R:Reichinger, D.J.; Arnot, D.E.; Tam, J.P.; Nussenzweig, V.; Enea, V.  
Mol. Cell. Biol. 6, 3965-3972, 1986  
A:Title: Circumsporozoite protein of Plasmodium berghei: gene cloning and identification  
A:Reference number: A25083; MUID:87089740  
A:Accession: A25083  
A:Molecule type: DNA  
A:Residues: 1-26, 'I', 28-68, 'PMLRR', 75-126, 'P', 128-134, 'PPNANDP', 135-332 <ETC>  
A:Cross-references: GB:M1435; MUID:q160245; PIDN:AAA29577.1; PID:q160246  
R:Weber, J.L.; Egan, J.E.; Lyon, J.A.; Wirtz, R.A.; Charoenvit, Y.; Maloy, W.L.; Hockmeyer, P.  
Exp. Parasitol. 63, 295-300, 1987  
A:Title: Plasmodium berghei: cloning of the circumsporozoite protein gene.  
A:Reference number: S13446; MUID:87218962  
A:Accession: S13446  
A:Molecule type: preliminary  
A:Status: preliminary  
A:Residues: 61-122, 'A', 124-332 <MEB>  
A:Cross-references: GB:M25445; MUID:q160177; PIDN:AAA29531.1; PID:q160178  
C:Comment: There are three distinct regions in the mature circumsporozoite protein, the obic membrane-anchoring sequence.  
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology  
C:Keywords: sporozoite; surface antigen; tandem repeat  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:124-332/Product: circumsporozoite protein #status predicted <MAT>  
F:94-189/Region: 8-residue repeats  
F:199-230/Region: 2-residue repeats  
F:258-310/Domain: thrombospondin type 1 repeat homology <THR1>  
  
Query Match 76.1%; Score 83; DB 1; Length 332;  
Best Local Similarity 61.9%; Pred. No. 8e-05;  
Matches 13; Conservative 7; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 DIEKICKMEKCSSEVFNVS 21  
||:||||:||||:||||:  
Db 298 DIDREICKMDKCSSEFNVS 318  
  
RESULT 8  
OZZOBK  
circumsporozoite protein precursor - Plasmodium berghei (strain ANKA clone 2.34L)  
N:Alternate names: sporozoite surface antigen  
C:Species: Plasmodium berghei  
C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Jul-1999  
C:Accession: S07873; S12571  
R:Lockyer, M.J.; Davies, C.S.; Subrtler, A.; Sindén, R.E.  
Nucleic Acids Res. 18, 376, 1990  
A:Title: Nucleotide sequence of the Plasmodium berghei circumsporozoite protein gene from  
A:Reference number: S07873; MUID:90221834  
A:Accession: S07873  
A:Molecule type: DNA  
A:Residues: 1-348 <LOC>  
A:Cross-references: EMBL:X17606  
R:Lockyer, M.J.  
submitted to the EMBL Data Library, November 1989  
A:Reference number: S12571  
A:Accession: S12571  
A:Molecule type: DNA  
A:Residues: 1-59, 'I', 61-81, 83-348 <LOC2>  
A:Cross-references: EMBL:X17606; MUID:q9784; PIDN:CAA35608.1; PID:q9785  
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology  
C:Keywords: tandem repeat  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-348/Product: circumsporozoite protein #status predicted <MAT>  
F:94-205/Region: 8-residue repeats  
F:215-247/Region: 2-residue repeats  
F:274-326/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 76.1%; Score 83; DB 1; Length 348;  
Best Local Similarity 61.9%; Pred. No. 8.3e-05;  
Matches 13; Conservative 7; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 DIEKICKMEKCSSEVFNVS 21  
||:||||:||||:||||:  
Db 314 DIDREICKMDKCSSEFNVS 334  
  
RESULT 9  
OZZOMY  
circumsporozoite protein precursor - Plasmodium yoelli  
N:Alternate names: sporozoite surface antigen  
C:Species: Plasmodium yoelli  
C:Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 16-Jul-1999  
C:Accession: A26271  
R:Leal, A.A.; de la Cruz, V.F.; Welsh, J.A.; Charoenvit, Y.; Maloy, W.L.; McCutchan, T.  
J. Biol. Chem. 262, 2937-2940, 1987  
A:Title: Structure of the gene encoding the circumsporozoite protein of Plasmodium yo  
A:Reference number: A26271; MUID:87137555  
A:Accession: A26271  
A:Molecule type: DNA  
A:Residues: 1-367 <LAL>  
A:Cross-references: GB:J02695; MUID:q160222; PIDN:AAA29558.1; PID:q160223  
C:Comment: There are three distinct regions in the mature circumsporozoite protein, t obic membrane-anchoring sequence.  
C:Comment: There are 15 copies of a 6-residue repeat and 8 copies of a 4-residue repe  
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology  
C:Keywords: sporozoite; surface antigen; tandem repeat  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-367/Product: circumsporozoite protein #status predicted <MAT>  
F:139-228/Region: 6-residue repeats (Q-G-P-G-A-P)  
F:229-260/Region: 4-residue repeats (Q-Q-P-P)  
F:293-345/Domain: thrombospondin type 1 repeat homology <THR1>  
  
Query Match 76.1%; Score 83; DB 1; Length 367;  
Best Local Similarity 61.9%; Pred. No. 8.7e-05;  
Matches 13; Conservative 7; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 DIEKICKMEKCSSEVFNVS 21  
||:||||:||||:||||:  
Db 333 DIDREICKMDKCSSEFNVS 353  
  
RESULT 10  
A54504  
circumsporozoite protein - Plasmodium malariae (strain Uganda 1-CDC)  
C:Species: Plasmodium malariae  
C:Date: 06-Oct-1994 #sequence\_revision 04-Nov-1994 #text\_change 20-Aug-1999  
C:Accession: A54504  
R:Leal, A.A.; de la Cruz, V.F.; Campbell, G.H.; Procell, P.M.; Collins, W.E.; McCutcha  
Mol. Biochem. Parasitol. 30, 291-294, 1988  
A:Title: Structure of the circumsporozoite gene of Plasmodium malariae.  
A:Reference number: A54504; MUID:89040027  
A:Accession: A54504  
A:Molecule type: DNA  
A:Residues: 1-429 <LAL>  
A:Cross-references: GB:J03992; MUID:q160220; PIDN:AAA29557.1; PID:q160221  
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology  
C:Keywords: tandem repeat  
F:354-407/Domain: thrombospondin type 1 repeat homology <THR1>  
  
Query Match 70.6%; Score 77; DB 2; Length 429;  
Best Local Similarity 57.1%; Pred. No. 0.00076;  
Matches 12; Conservative 7; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 DIEKICKMEKCSSEVFNVS 21  
||:||||:||||:||||:  
Db 395 DLEFICSLDKCSSEFNVS 415

```

RESULT      11
A60610
Circumsporozoite protein precursor - Plasmodium brasilianum
C:Species: Plasmodium brasilianum
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Aug-1999
C:Accession: A60610; A28615
R:di Giovanni, L.; Cochrane, A.H.; Enea, V.
Exp. Parasitol. 70, 373-381, 1990
A>Title: On the evolutionary history of the circumsporozoite protein in plasmodia.
A:Reference number: A60610; MUID:90214818
A:Accession: A60610
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-485 <DIA>
J:Ital., A.A.: de la Cruz, V.F.; Collins, W.E.; Campbell, G.H.; Procell, P.M.; McCutchan, J.T. Biol. Chem. 263, 5495-5498, 1988
A>Title: Circumsporozoite protein gene from Plasmodium brasilianum. Animal reservoirs fo
A:Reference number: A28615; MUID:86186854
A:Accession: A28615
A:Molecule type: DNA
A:Residues: 93-485 <IAL>
A:Cross-references: GB:j03203; MID:g160212; PIDN:AAA29553.1; PID:g160213
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
C:Keywords: sporozoite; surface antigen; tandem repeat
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-485/Product: circumsporozoite protein #status predicted <MAT>
F:114-369/Region: 4-residue repeats
F:410-463/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match          70.6%; Score 77; DB 2; Length 485;
Best Local Similarity 57.1%; Pred. No. 0.00085; Indels    0; Gaps   0;
Matches 12; Conservative 7; Mismatches 2;

QY      1 DIEKKICKMEKCSVFNVNS 21
       I::II::IIIII::IIII::
DB     451 DLEETVCITDKCAIFNVNSN 471

RESULT      12
OZ2OAB
circumsporozoite protein precursor - plasmodium cynomolg1 (strain Berok)
N:Alternate names: major sporozoite surface antigen
C:Species: Plasmodium cynomolg1
C>Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 07-Nov-1997
C:Accession: D26255
R:Gallinski, M.R.; Arnott, D.E.; Cochran, A.H.; Barnwell, J.W.; Nussenzweig, R.S.; Enea, C.I.
A>Title: The circumsporozoite gene of the Plasmodium cynomolg1 complex.
A:Reference number: A90889; MUID:87102878
A:Accession: D26255
A:Molecule type: DNA
A:Residues: 1-378 <GAL>
C:Comment: There are three distinct regions in the mature circumsporozoite protein, the obic membrane anchoring sequence.
C:Comment: There are 10 tandem copies of a 9-residue repeat (preceded by a 6-residue in C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
C:Keywords: sporozoite; surface antigen; tandem repeat
F:1-15/Domain: signal sequence #status predicted <SIG>
F:20-378/P:roduct: circumsporozoite protein #status predicted <MAT>
F:97-192/Region: 9-residue repeats
F:193-268/Region: 16-residue repeats
F:303-356/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match          65.1%; Score 71; DB 1; Length 378;
Best Local Similarity 47.6%; Pred. No. 0.0051; Indels    0; Gaps   0;
Matches 10; Conservative 8; Mismatches 3;

QY      1 DIEKKICKMEKCSVFNVNS 21
       I::::I::II::IIII::
DB     344, DLEETVCTDKACAGFNVSIN 364
```

```

RESULT 13
OZZOAL
circumsporozoite protein precursor - Plasmodium cynomolgi (strain London)
N:Alternate names: major sporozoite surface antigen
C:Species: Plasmodium cynomolgi
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 07-Nov-1997
C:Accession: A26255
R:Galinski, M.R.; Arnott, D.E.; Cochrane, A.H.; Barnwell, J.W.; Nussenzweig, R.S.; Enn
Cell 48; 311-319, 1987
A:Title: The circumsporozoite gene of the Plasmodium cynomolgi complex.
A:Reference number: A90889; MUID:87102878
A:Accession: A26255
A:Molecule type: DNA
A:Residues: 1-378 <GAL>
C:Comment: There are three distinct regions in the mature circumsporozoite protein, t
obic membrane-anchoring sequence.
C:Comment: There are 19 tandem copies of a 6-residue repeat and 6 copies of an 11-res
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
C:Keywords: sporozoite; surface antigen; tandem repeat
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-378/Product: circumsporozoite protein #status predicted <MAT>
F:98-211/Region: 6-residue repeats
F:212-277/Region: 11-residue repeats
F:303-356/Domain: thrombospondin type 1 repeat homology <THRI>

Query Match 65.1%; Score 71; DB 1; Length 378;
Best Local Similarity 47.6%; Pred. No. 0.0051; 3; Indels 0; Gaps 0;
Matches 10; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

OY 1 DIEKICKMEKCSSVFNVNS 21
|:|::|:|::|:|::|:|::|:|::|:|:
Db 344 DIETEVCTMDKAGIFNVNS 364

RESULT 14
OZZOAS
circumsporozoite protein precursor - Plasmodium cynomolgi (strain Ceylon)
N:Alternate names: major sporozoite surface antigen
C:Species: Plasmodium cynomolgi
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 07-Nov-1997
C:Accession: C26255
R:Galinski, M.R.; Arnott, D.E.; Cochrane, A.H.; Barnwell, J.W.; Nussenzweig, R.S.; Enn
Cell 48; 311-319, 1987
A:Title: The circumsporozoite gene of the Plasmodium cynomolgi complex.
A:Reference number: A90889; MUID:87102878
A:Accession: C26255
A:Molecule type: DNA
A:Residues: 1-398 <GAL>
C:Comment: There are three distinct regions in the mature circumsporozoite protein, t
obic membrane-anchoring sequence.
C:Comment: There are 16 tandem copies of a 9-residue repeat and 3 copies of a 17-resi
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
C:Keywords: sporozoite; surface antigen; tandem repeat
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-398/Product: circumsporozoite protein #status predicted <MAT>
F:97-240/Region: 9-residue repeats
F:241-291/Region: 17-residue repeats
F:323-376/Domain: thrombospondin type 1 repeat homology <THRI>

Query Match 65.1%; Score 71; DB 1; Length 398;
Best Local Similarity 47.6%; Pred. No. 0.0054; 3; Indels 0; Gaps 0;
Matches 10; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

OY 1 DIEKICKMEKCSSVFNVNS 21
|:|::|:|::|:|::|:|::|:|::|:|:
Db 364 DIETEVCTMDKAGIFNVNS 384

```



OZZOAC  
 Circumsporozoite protein precursor - Plasmodium cynomolgi (strain Gombak)  
 N:Alternate names: major sporozoite surface antigen  
 C:Species: Plasmodium cynomolgi  
 C:Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 07-Nov-1997  
 C:Accession: E26255  
 R:Galinski, M.R.; Annot, D.E.; Cochran, A.H.; Barnwell, J.W.; Nussenzweig, R.S.; Enea, Cell 48, 311-319, 1987  
 A:Title: The circumsporozoite gene of the Plasmodium cynomolgi complex.  
 A:Reference number: A90889; MUID:87102878  
 A:Accession: E26255  
 A:Molecule type: DNA  
 A:Residues: 1-401 <GAL>  
 C:Comment: There are three distinct regions in the mature circumsporozoite protein, the obic membrane-anchoring sequence.  
 C:Comment: There are 17 tandem copies of the 11-residue repeat D/G-A-A-A-A-G-G-G-G-N.  
 C:Superfamily: Circumsporozoite protein; thrombospondin type 1 repeat homology  
 C:Keywords: sporozoite; surface antigen; tandem repeat  
 F:1-19/Domain: signal sequence #status predicted <Sig>  
 F:20-401/Product: circumsporozoite protein #status predicted <Mat>  
 F:98-278/Region: 11-residue repeats  
 F:326-379/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 65.1%; Score 71; DB 1; Length 401;  
 Best Local Similarity 47.6%; Pred. No. 0.0054;  
 Matches 10; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIEKKICKMEKCSSVFNVNS 21  
 I: I : I I : I I : I I I I :  
 Db 367 DLETEVCTMDKCAGIFNVNS 387

Search completed: January 29, 2002, 10:26:36  
 Job time: 647 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 11:13:47 ; Search time 80.65 Seconds  
(without alignments)  
8.638 Million cell updates/sec

Title: US-09-763-397A-20

Perfect score: 96

Sequence: 1 NEREDERTLTKEYEDIVLK 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 3664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SWISSProt\_39:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	96	100.0	1435	1	EBAL_PLAFC
2	49	51.0	1435	1	BAM_DROME
3	49	51.0	598	1	YDM3_SCHPO
4	46	47.9	213	1	VP09_VACCC
5	46	47.9	213	1	VP09_VACCV
6	46	47.9	213	1	VP09_VARY
7	46	47.9	453	1	TBA1_NEUCR
8	45	46.9	513	1	GAL7_BACSU
9	45	46.9	1282	1	TP2M_DICDI
10	44	45.8	332	1	LDHD_LACDE
11	44	45.8	451	1	TBA2_HOMAM
12	44	45.8	985	1	NAH1_YEAST
13	43.5	44.3	731	1	BAF1_YEAST
14	43	44.8	943	1	DIP2_YEAST
15	42	43.8	208	1	RL4_MYCA
16	42	43.8	239	1	FRDB_WOLSU
17	42	43.8	274	1	Y059_CAEEL
18	42	43.8	603	1	HEM1_CHICK
19	41	42.7	101	1	YT01_MYCN
20	41	42.7	196	1	CAIE_ECOLI
21	41	42.7	450	1	TBA_NOTVI
22	41	42.7	463	1	CMGA_MOUSE
23	41	42.7	466	1	CMGA_MOUSE
24	41	42.7	668	1	CMGA_MOUSE
25	41	42.7	668	1	CMGA_MOUSE
26	41	42.7	711	1	SMC7_SCHMA
27	41	42.7	776	1	YOFF_BACSU
28	41	42.7	1770	1	TOP1_RICPR
29	40.5	42.2	457	1	R115_YEAST
30	40	41.7	240	1	CMGA_HUMAN
31	40	41.7	347	1	TBA_OCTVU
32	40	41.7	353	1	YCEG_HAEIN
33	40	41.7	393	1	BMP2_CHICK

34	40	41.7	394	1	BMP2_MOUSE
35	40	41.7	395	1	BMP2_RABIT
36	40	41.7	396	1	BMP2_DAMDA
37	40	41.7	396	1	BMP2_HUMAN
38	40	41.7	398	1	BMPA_XENLA
39	40	41.7	398	1	BMPB_XENLA
40	40	41.7	412	1	TBA1_CHICK
41	40	41.7	444	1	TBA_ONCKE
42	40	41.7	448	1	TBA4_HUMAN
43	40	41.7	448	1	TBA5_CHICK
44	40	41.7	449	1	CMGA_BOVIN
45	40	41.7	449	1	TBA6_MOUSE

## ALIGNMENTS

RESULT 1	ID	EBAL_PLAFC	STANDARD:	PRT:	1435 AA.
AC	P19214:	01-NOV-1990 (Rel. 16, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	01-FEB-1996 (Rel. 33, Last annotation update)				
DE	ERYTHROCYTE-BINDING ANTIGEN EBA-175.				
OS	Plasmodium falciparum (isolate Camp / Malaysia).				
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.				
OX	NCBI_TaxID=5835;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90377299; PubMed=2204835;				
RA	Sim B.K.L.:				
RT	"Sequence conservation of a functional domain of erythrocyte binding antigen I/5 in Plasmodium falciparum.";				
RL	Mol. Biochem. Parasitol. 41:293-296(1990).				
CC	-----				
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CC	-----				
DR	EMBL: X52524; CAA36756.1; -.				
DR	PIR: S11561; S11561.				
KW	Antigen.				
FT	DOMAIN 159 1104				
FT	ESSENTIAL FOR BINDING TO ERYTHROCYTES.				
FT	VARIANT 1031 1031 E -> V (IN STRAINS FCR-3 AND ITC).				
FT	SEQUENCE 1435 AA; 167389 MW; 32A4309021BIC3D6 CRC64;				
SQ					
Query Match 100.0%; Score 96; DB 1; Length 1435;					
Best Local Similarity 100.0%; Pred. No. 1.5e+06;					
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Oy	1	NEREDERTLTKEYEDIVLK 19			
Db	1069	NEREDERTLTKEYEDIVLK 1087			
RESULT 2					
BAM_DROME					
ID	BAM_DROME	STANDARD:	PRT:	442 AA.	
AC	P22745: O9BVO:				
DT	01-AUG-1991 (Rel. 19, Created)				
DT	20-AUG-2001 (Rel. 40, Last sequence update)				
DT	20-AUG-2001 (Rel. 40, Last annotation update)				
DE	BAG-OF-MARPLES PROTEIN (BAM PROTEIN).				
GN	BAM OR CG10422.				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				

CC Pterygota:Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
CC Phlebotomidae; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
[1]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RP STRAIN=FS(3)NEO61; TISSUE=Ovary;  
RC MEDLINE=911126627; PubMed=22796598;  
RX McKearin D.M., Spradling A.C.;  
RT "Bag-of-marbles: a Drosophila gene required to initiate both male and  
RT female gametogenesis";  
RL Genes Dev. 4:2242-2251(1990).  
[2]  
RP REVISIONS TO 99-113.  
RP McKearin D.M.;  
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
[3]  
RP SEQUENCE FROM N.A.  
RP STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sulten G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blaise J.R.G., Champs M., Pfeiffer B.D.,  
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Dou P.L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Folsler C., Gaboriellian A.E., Gar N.S., Gelbart W.M., Glasser K.,  
RA Glodex A., Gong F., Gorrell J.R., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegwan C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kalp D., Lai Z.,  
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector A.C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong E.W., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
CC -I- FUNCTION: REQUIRED TO INITIATE BOTH MALE AND FEMALE GAMETOGENESIS.  
CC MAY REGULATE CYSTOBLAST CELL DIVISIONS.  
CC -I- TISSUE SPECIFICITY: IN CYSTOBLASTS AND/OR VERY EARLY CYSTOCYTES IN  
CC OVARY AND TESTIS.  
CC -I- SIMILARITY: LOW, WITH THE DROSOPHILA OVARIAN TUMOR GENE PROTEIN.  
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CC  
CC EMBL: X556202; CAA39662.1; -  
CC EMBL: AE003751; AAF56427.1; -

DR	PIR: A36469; A36466.	
DR	flyBase; FBgn0000158; bam.	
FT	DOMAIN 402 434	GLU/SER/PRO/THR-RICH (PEST REGION)
FT	CONFLICT 239 239	R -> S (IN REF. 1).
FT	CONFLICT 439 439	A -> A (IN REF. 1).
SQ	SEQUENCE 442 AA; 50275 MW; D2FE2BECFCA9FE54 CRC64;	

Query Match	51.0%;	Score 49;	DB 1;	Length 442;
Best Local Similarity	66.7%;	Pred. No. 4.4;		
Matches 10;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;

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QY      1 NEREDERTLKEYED 15
          || || | | |||
Db      35 NENEDPRKATCEYED 49
```

RESULT	3	
YDM3_SCHPO		
ID	YDM3_SCHPO	STANDARD;
		PRT;
		598 AA

DE HYPOTHETICAL 67.7 KDA PROTEIN C23C11.03 IN CHROMOSOME I  
DN SPAC23C11.03.

0C Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes  
0C Schizosaccharomycetales; Schizosaccharomycetaceae;  
0C Schizosaccharomycetes.  
NCBI\_TaxID=4896;  
OX

RP SEQUENCE FROM N.A.  
RC STRAIN=972:  
RA Brown D., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.,  
RL Submitted (AUG-1997) to the EMBL/Genbank/DBD databases.  
CC - SIMILARITY: BELONGS TO THE MP10 FAMILY.

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Accession	Protein	Length (aa)	MD5
U00001	EMBL:U00001; CAB1150.1; -	240	POLY-LYS.
U00001	Hypothetical protein.	240	POLY-LYS.
U00001	DOMAIN	237	POLY-PRO.
U00001	FT	462	POLY-ARG.
U00001	DOMAIN	532	POLY-ARG.
U00001	FT	538	POLY-ARG.
U00001	SEQUENCE	598 AA; 67707 MW; 36433BA1106FEF99 CRC64	

Query Match	51.0%;	Score 49;	DB 1;	Length 598;
Best Local Similarity	47.4%;	Pred. No. 6.2;		
Matches	9;	Conservative	5;	Mismatches 5; Indels 0; Gaps 0;

```
QY      1 NEREDERTLTKEYEDIVLK 19
         || : : | : | | : ||
Db      401 NENKSQRSLAEYEYEEFLK 419
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RESULT	4		
ID	VD09_VACCC	STANDARD;	PRT; 213 AA.
VD09_VACCC			

DT 01-FEB-1991 (Rel. 17, last sequence update)  
DT 20-AUG-2001 (Rel. 40, last annotation update)  
DE PROTEIN D9.

OS Vaccinia virus (strain Copenhagen).

```

OC  viruses: dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC  Orthopoxvirus.
OX  NCBI_Taxid=10249;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=91021027; PubMed=2219722;
RA  Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Wanslow J.P.,
RT  Paoletti E.;
RT  "The complete DNA sequence of vaccinia virus.";
RL  Virology 179:247-266(1990).
RN  [2]
RP  COMPLETE GENOME.
RA  Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Wanslow J.P.,
RT  Paoletti E.;
RT  "Appendix to 'The complete DNA sequence of vaccinia virus.'";
RL  Virology 179:517-563(1990).
CC  -1- SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY.
CC  -----
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CC  -----
DR  EMBL: M35027; AAA48108.1; -
DR  PIR: H42515; H42515.
DR  InterPro: IPR000086; NUDIX_hydrolase.
DR  InterPro: IPR003300; Viral_VD9.
DR  Pfam: PF00293; mult; 1.
DR  PRINTS: PR00502; MUTDOMAIN.
DR  PROSITE: PS00893; NUDIX; 1.
KW  Hydrolase.
FT  DOMAIN 111 132 NUDIX BOX.
FT  SEQUENCE 213 AA; 25024 MW; 747688883C43EF7E CRC64;

Query Match 47.9%; Score 46; DB 1: Length 213;
Best Local Similarity 44.4%; Pred. No. 5.6;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 2 EREDERTLTKKEYEDIVLK 19
Db 129 EESDERITVKEFGNVILK 146
1 111 11: :::11

RESULT 5
VD09_VACCV STANDARD; PRT; 213 AA.
ID VD09_VACCV
AC P04311;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROTEIN D9.
GN D9R.
OS Vaccinia virus (strain WR).
OC Viruses: dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_Taxid=10254;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86291159; PubMed=3739227;
RA Niles E.G., Condit R.C., Caro P., Davidson K., Matusick L., Seto J.;
RT "Nucleotide sequence and genetic map of the 16-kb vaccinia virus
RT HindIII D fragment.";
RL Virology 153:96-112(1986).
CC -1- SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY.
CC -----
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CC -----
DR  EMBL: M15058; AAA48265.1; -
DR  PIR: A03885; Q0VZ15.
DR  InterPro: IPR000086; NUDIX_hydrolase.
DR  InterPro: IPR003300; Viral_VD9.
DR  Pfam: PF00293; mult; 1.
DR  PRINTS: PR00502; MUTDOMAIN.
DR  PROSITE: PS00893; NUDIX; 1.
KW Hydrolase.
FT  DOMAIN 111 132 NUDIX BOX.
FT  SEQUENCE 213 AA; 24994 MW; 306288883C5899A5 CRC64;

Query Match 47.9%; Score 46; DB 1: Length 213;
Best Local Similarity 44.4%; Pred. No. 5.6;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 2 EREDERTLTKKEYEDIVLK 19
Db 129 EESDERITVKEFGNVILK 146
1 111 11: :::11

RESULT 6
VD09_VARY STANDARD; PRT; 213 AA.
ID VD09_VARY
AC P33070;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROTEIN D9.
GN D9R OR F9R.
OS Variola virus.
OC Viruses: dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_Taxid=10255;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=INDIA-1967 / ISOLATE IND3;
RX MEDLINE=93190624; PubMed=8383392;
RA Shchelkunov S.N., Blinov V.M., Tolmenin A.V., Marenikova S.S.,
RA Kolykhalov A.A., Frolov I.V., Chizhikov V.E., Gytarov V.V.,
RA Gashikov P.V., Belanov E.F., Belavin P.A., Resenchuk S.M.,
RA Andzharidze O.G., Sandakhchley L.S.;
RT "Nucleotide sequence analysis of variola virus HindIII M, L, I genome
RT fragments.";
RL Virus Res. 27:25-35(1993).
RN [2]
RP COMPLETE GENOME.
RX STRAIN=INDIA-1967 / ISOLATE IND3;
RX MEDLINE=93202281; PubMed=8384129;
RA Shchelkunov S.N., Blinov V.M., Sandakhchley L.S.;
RT "Genes of variola and vaccinia viruses necessary to overcome the host
RT protective mechanisms.";
RL FEBS Lett. 319:80-83(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=BANGLADESH-1975;
RX MEDLINE=94088747; PubMed=8264798;
RA Massung R.F., Esposito J.J., Liu L., Qi J., Utterback T.R.,
RA Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
RA Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
RA Venter C.J.;
RT "Potential virulence determinants in terminal regions of variola
RT smallpox virus genome.";
RL Nature 366:748-751(1993).
CC -1- SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY.
CC -----
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RESULT 9  
ID TP2M\_DICDI STANDARD: PRT: 1282 AA.  
AC P90520:  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE DNA TOPOISOMERASE II, MITOCHONDRIAL PRECURSOR (EC 5.99.1.3).  
GN TOPI OR TOPIA.  
OS Dictyostelium discoideum (Slime mold).  
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.  
OX NCBI\_TaxID=44689;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AX3;  
RX MEDLINE=97320633; PubMed=9177484;  
RA Komori K., Kuroe K., Yanagisawa K., Tanaka Y.;  
RT "Cloning and characterization of the gene encoding a mitochondrially  
RT localized DNA topoisomerase II in Dictyostelium discoideum. Western  
RT blot analysis."  
RL Blochim. Biophys. Acta 1352:63-72(1997).  
CC -1- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT  
CC BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II  
CC MAKES DOUBLE-STRAND BREAKS (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING  
CC OF DOUBLE-STRAND DNA.  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.  
CC -1- DEVELOPMENTAL STAGE: PRESENT IN GROWTH PHASE AND DURING  
CC DEVELOPMENT, ALTHOUGH LEVELS DECLINED AS DEVELOPMENT PROCEEDED.  
CC -1- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.  
CC -----  
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CC -----  
CC  
DR EMBL: D82024; BAA11510.1; -.  
DR Dictydb: DD05117; TOPB.  
DR InterPro: IPR001241; DNA\_topoisomII.  
DR InterPro: IPR002305; DNA\_topoisomII.  
DR InterPro: IPR003594; HATPase\_c.  
DR Pfam: PF00204; DNA\_topoisomII; 2.  
DR Pfam: PF00521; DNA\_topoisomII; 1.  
DR Pfam: PF02518; HATPase\_c; 1.  
DR PRINTS: PR00418; TP12FAMILY.  
DR PRINTS: PR01158; TOPISMRASEII.  
DR PRODOM: PD000616; DNA\_topoisomII; 1.  
DR SMART: SM00387; HATPase\_c; 1.  
DR SMART: SM00433; TOP2c; 1.  
DR SMART: SM00434; TOP2c; 1.  
DR PROSITE: PS00177; TOPOISOMERASE II; 1.  
KW Isomerase; Topoisomerase; DNA-binding; ATP-binding;  
KW Mitochondrion; Transist peptide.  
FT TRANSIT 1 35 MITOCHONDRION (POTENTIAL).  
FT CHAIN 36 1282 DNA TOPOISOMERASE II.  
FT NP\_BIND 253 258 ATP (POTENTIAL).  
FT ACT\_SITE 899 899 DNA CLEAVAGE (BY SIMILARITY).  
FT DOMAIN 147 154 POLY-THR.  
FT DOMAIN 1252 1256 POLY-SER.  
FT DOMAIN 1260 1265 POLY-SER.  
SQ SEQUENCE 1282 AA; 145866 MW; 7E21DEBF3D069951 CRC64;

Query Match 46.9%; Score 45; DB 1; Length 1282;  
Best Local Similarity 47.4%; Pred. No. 56;  
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
Oy 1 NEREDERTLTKEYEDIVLK 19

DB 75 NEKISEKTTTRKEDIYOK 93  
||:|:|:|:|  
RESULT 10  
ID LHDH\_LACDE STANDARD: PRT: 332 AA.  
AC P26297;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE D-LACTATE DEHYDROGENASE (EC 1.1.1.28) (D-LDH).  
GN LDHA.  
OS Lactobacillus delbrueckii (subsp. bulgaricus).  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;  
OC Lactobacillus.  
OX NCBI\_TaxID=1585;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NCIB 11778;  
RX MEDLINE=92008688; PubMed=1915894;  
RA Bernard N., Ferrain T., Garmyn D., Hols P., Delcour J.;  
RT "Cloning of the D-lactate dehydrogenase gene from Lactobacillus  
RT delbrueckii subsp. bulgaricus by complementation in Escherichia  
RT coli."  
RL FEBS Lett. 290:61-64(1991).  
RN [2]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE=92235079; PubMed=1569100;  
RA Kochhar S., Hunziker P., Leong-Morgenthaler P.M., Hottinger H.;  
RT "Primary structure, physicochemical properties, and chemical  
RT modification of NAD(+)-dependent D-lactate dehydrogenase. Evidence  
RT for the presence of Arg-235, His-303, Tyr-101, and Trp-19 at or near  
RT the active site."  
RL J. Biol. Chem. 267:8499-8513(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92304298; PubMed=1610363;  
RA Kochhar S., Chuard N., Hottinger H.;  
RT "Cloning and overexpression of the Lactobacillus bulgaricus NAD(+)-  
RT dependent D-lactate dehydrogenase gene in Escherichia  
RT coli: purification and characterization of the recombinant enzyme."  
RL Biochem. Biophys. Res. Commun. 185:705-712(1992).  
RN [4]  
RP SIMILARITY TO OTHER ENZYMES OF THIS FAMILY.  
RX MEDLINE=92231983; PubMed=1567457;  
RA Kochhar S., Hunziker P., Leong-Morgenthaler P.M., Hottinger H.;  
RT "Evolutionary relationship of NAD(+)-dependent D-lactate  
RT dehydrogenase: comparison of primary structure of 2-hydroxy acid  
RT dehydrogenases."  
RL Biochem. Biophys. Res. Commun. 184:60-66(1992).  
RN [5]  
RP MUTAGENESIS OF HIS-205; ARG-235; ASP-259; GLU-264 AND HIS-296.  
RX MEDLINE=97217445; PubMed=9063466;  
RA Bernard N., Johnson K., Geipl J.L., Alvarez J.A., Ferrain T.,  
RA Garmyn D., Hols P., Cortes A., Clarke A.R., Holbrook J.J., Delcour J.;  
RT "D-2-hydroxy-4-methylvalerate dehydrogenase from Lactobacillus  
RT delbrueckii subsp. bulgaricus. II. Mutagenic analysis of  
RT catalytically important residues."  
RL Eur. J. Biochem. 244:213-219(1997).  
RN [6]  
RP 3D-STRUCTURE MODELING.  
RA Vinals C., de Bolle X., Deleureux E., Feytmans E.;  
RP Submitted (JAN-1995) to the EMBL/Genbank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: D-LACTATE + NAD(+) -> PYRUVATE + NADH.  
CC -1- SUBUNIT: HOMODIMER.  
CC -1- SIMILARITY: BELONGS TO THE D-ISOMER SPECIFIC 2-HYDROXYACID  
CC DEHYDROGENASES FAMILY.  
CC -----  
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DR EMBL: X60220; CAA42781.1; -  
DR EMBL: M65224; AAA25246.1; -  
DR PIR: S17556; S17556.  
DR PIR: JN0245; JN0245.  
DR PIR: A38094; A38094.  
DR PDB: 1DLD; 31-MAR-95.  
DR InterPro: IPR002162; D\_2\_hydroxyacid\_DH.  
DR Pfam: PF00389; 2-Hacid\_DH.1.  
DR PROSITE: PS00065; D\_2-HYDROXYACID\_DH.1; 1.  
DR PROSITE: PS00670; D\_2-HYDROXYACID\_DH.2; 1.  
DR PROSITE: PS00671; D\_2-HYDROXYACID\_DH.3; 1.  
KW Oxidoreductase; NAD; 3D-structure.  
FT INIT MET 0  
FT NP\_BIND 147 175 NAD (BY SIMILARITY).  
FT ACT\_SITE 235 235 SUBSTRATE-BINDING (BY SIMILARITY).  
FT ACT\_SITE 264 264 BY SIMILARITY.  
FT ACT\_SITE 296 296 BY SIMILARITY.  
FT MUTAGEN 205 205 H->Q: INCREASE OF ACTIVITY.  
FT MUTAGEN 235 235 R->K: DECREASE OF ACTIVITY.  
FT MUTAGEN 259 259 D->N: DECREASE OF ACTIVITY.  
FT MUTAGEN 264 264 E->Q: DECREASE OF ACTIVITY.  
FT MUTAGEN 296 296 H->Q: 90% LOSS OF ACTIVITY.  
FT CONFLICT 40 40 A -> V (IN REF. 1).  
FT CONFLICT 116 116 R -> A (IN REF. 1).  
FT CONFLICT 121 121 A -> D (IN REF. 1).  
FT CONFLICT 151 151 V -> I (IN REF. 1).  
FT CONFLICT 173 173 A -> T (IN REF. 1).  
FT CONFLICT 219 219 K -> E (IN REF. 1).  
FT CONFLICT 253 253 V -> I (IN REF. 1).  
FT CONFLICT 267 267 V -> I (IN REF. 1).  
FT CONFLICT 272 272 R -> W (IN REF. 1).  
SQ SEQUENCE 332 AA; 36773 MW; D776CA0746589449 CRC64;

Query Match 45.8%; Score 44; DB 1; Length 332;  
Best Local Similarity 61.5%; Pred. No. 18;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
OY 3 REDERTLTKREVED 15  
Db 9 REDEKPLKEMED 21

RESULT 11  
TBA2\_HOMAM STANDARD; PRT; 451 AA.  
AC 094570;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE TUBULIN ALPHA-2 CHAIN (ALPHA-TI TUBULIN).  
OS Homarus americanus (American lobster).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
OC Nephropoidea; Nephropidae; Homarus.  
OX NCBI\_Taxid=6706;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96257217; PubMed=8666270;  
RA Demers D.M., Metcalf A.E., Talbot P., Hyman B.C.;  
RT "Multiple lobster tubulin isoforms are encoded by a single gene  
family";  
RL Gene 171:185-191(1996).  
CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT  
CC BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BETA  
CC CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.  
CC -1- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.  
CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.

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DR EMBL: U66318; AAB07481.1; -  
DR InterPro: IPR000217; Tubulin.  
DR InterPro: IPR003008; Tubulin\_Ftsz.  
DR Pfam: PF00091; tubulin; 1.  
DR PRINTS: PR01161; TUBULIN.  
DR PRINTS: PR01162; ALPHATUBULIN.  
DR PROSITE: PS00227; TUBULIN; 1.  
KW Microtubules; GTP-binding; Multigene family.  
FT NP\_BIND 142 148 GTP (POTENTIAL).  
FT SITE 451 451 INVOLVED IN POLYMERIZATION.  
SQ SEQUENCE 451 AA; 50250 MW; 5D7751B2330358B6 CRC64;

Query Match 45.8%; Score 44; DB 1; Length 451;  
Best Local Similarity 57.1%; Pred. No. 25;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
OY 3 REDERTLTKREVED 16  
Db 422 REDATLTKREVED 435

RESULT 12  
NAH1\_YEAST STANDARD; PRT; 985 AA.  
ID NAH1\_YEAST  
AC 099271;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE NA(+)/H(+) ANTI-PORTER.  
GN NAH1 OR YLR138W OR L3149 OR L9606.4.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_Taxid=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=5288C / AB972;  
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,  
RA Favell A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,  
RA Hallsworth K., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,  
RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,  
RA Taich A., Trevasik E., Vignati D., Wilcox L., Woldman P., Vaudin M.,  
RA Wilson R., Waterston R.,  
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=5288C;  
RA Delius H., Hedling U.;  
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 145-985 FROM N.A.  
RX Rieger M., Mueller-Auer S., Brueckner M.;  
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: SODIUM EXPORT FROM CELL. TAKES UP EXTERNAL PROTONS IN  
CC EXCHANGE FOR INTERNAL SODIUM IONS (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC -1- SIMILARITY: BELONGS TO THE FUNGAL NA(+)/H(+) EXCHANGER FAMILY.  
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CC
DR EMBL: U53881; AAB82392.1; -.
DR EMBL: X91258; CAA62653.1; -.
DR EMBL: Z73310; CAA97709.1; -.
DR EMBL: Z73311; CAA97711.1; -.
DR SGD: S0004128; NHA1
DR InterPro: IPR000676; NaH_Exchange.
DR Pfam: PF00999; Na_H_Exchange; 1.
KW Transmembrane; Glycoprotein; Sodium transport; Transport; Symport.
FT TRANSMEM 13 33
FT TRANSMEM 37 57 POTENTIAL.
FT TRANSMEM 71 91 POTENTIAL.
FT TRANSMEM 106 126 POTENTIAL.
FT TRANSMEM 129 149 POTENTIAL.
FT TRANSMEM 177 197 POTENTIAL.
FT TRANSMEM 204 224 POTENTIAL.
FT TRANSMEM 245 265 POTENTIAL.
FT TRANSMEM 295 315 POTENTIAL.
FT TRANSMEM 320 340 POTENTIAL.
FT TRANSMEM 362 382 POTENTIAL.
FT TRANSMEM 411 431 POTENTIAL.
SQ SEQUENCE 985 AA; 109369 MW; AD0B86D483DCDD89 CRC64;

Query Match 45.8%; Score 44; DB 1; Length 985;
Best Local Similarity 60.0%; Pred. No. 60;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 NEREDERTLTREYED 15
   : | | | | | | |
Db 616 DEEDEYTPREKEYSD 630

RESULT 13
BAF1_YEAST STANDARD; PRT; 731 AA.
ID BAF1_YEAST
AC P14164;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1980 (Rel. 16, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE TRANSCRIPTION FACTOR BAF1 (ARIS BINDING FACTOR 1) (PROTEIN ABL1)
DE (BIDIRECTIONALLY ACTING FACTOR) (SFB-B) (DNA REPLICATION ENHANCER-
DE BINDING PROTEIN OBF1).
GN BAF1 OR ABL1 OR OBF1 OR YKL112W OR YKL505.
GS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90069559; PubMed=2511628;
RA Diffley J.F.X., Stillman B.;
RT "Similarity between the transcriptional silencer binding proteins
RT ABL1 and RAP1.";
RL Science 246:1034-1038(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90152338; PubMed=2620828;
RA Rhode P.R., Sweder K.S., Oegema K.F., Campbell J.L.;
RT "The gene encoding ARS-binding factor I is essential for the
RT viability of yeast.";
RL Genes Dev. 3:1926-1939(1989).
RN [3]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 128-154 AND 535-555.
RX MEDLINE=90076149; PubMed=2686983;
RA Halfter H., Kavey B., Vandeckerckhove J., Kiefer F., Gallwitz D.;
RT "Sequence, expression and mutational analysis of BAF1, a
RT transcriptional activator and ARS1-binding protein of the yeast
RL Saccharomyces cerevisiae.";
RL EMBO J. 8:4265-4272(1989).
RN [4]

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RP SEQUENCE FROM N.A., AND PHOSPHORYLATION.
RX MEDLINE-91239512; PubMed-2034654;
RA Francsconi S.C., Eisenberg S.;
RT "The multifunctional protein OBP1 is phosphorylated at serine and
RL theoneine residues in Saccharomyces cerevisiae.";
RN Proc. Natl. Acad. Sci. U.S.A. 88:4089-4093(1991).
RN [5]
RN SEQUENCE FROM N.A.
RP MEDLINE-92221689; PubMed-1561835;
RA Jacquier A., Legrain P., Dujon B.;
RT "Sequence of a 10.7 kb segment of yeast chromosome XI identifies the
RN APR1 and the BAP1 loci and reveals one tRNA gene and several new open
RN reading frames including homologs to RAD2 and Kinases.";
RN yeast 8:121-132(1992).
RN [6]
RN SEQUENCE OF 585-731 FROM N.A.
RP MEDLINE-94344141; PubMed-8065362;
RA Butler A.R., White J.H., Polawito Y., Edlin A., Gardiner D.,
RN Stark M.J.R.;
RT "Two Saccharomyces cerevisiae genes which control sensitivity to G1
RN arrest induced by Kluyveromyces fragilis toxin*";
RN Mol. Cell. Biol. 14:6306-6316(1994).
RN CC -1- FUNCTION: TRANS-ACTING FACTOR IN THE REGULATION OF TRANSCRIPTION
RN AND IN DNA REPLICATION. INVOLVED IN THE TRANSCRIPTION ACTIVATION
RN OF A SUBSET OF RIBOSOMAL PROTEINS GENES. BINDS THE ARS-ELEMENTS
RN FOUND IN MANY PROMOTERS. BINDS TO THE SEQUENCE 5'-TCN(7)ACG-3'.
RN CC -1- SUBCELLULAR LOCATION: NUCLEUS.
RN CC -1-1- SIMILARITY: STRONG TO KLUYVEROMYCES ABE1, AND LOCAL TO YEAST RAP1.
RN CC
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RN CC -----
RN CC EMBL: X16385; CAA34421.1; -
RN DR EMBL: X51654; CAA35966.1; -
RN DR EMBL: M29067; AAA66511.1; -
RN DR EMBL: M63578; AAA34823.1; -
RN DR EMBL: S93804; AAB22002.1; -
RN DR EMBL: Z28111; CAA81951.1; -
RN DR EMBL: X77511; CAA54647.1; -
RN DR PIR: S29870; S29870.
RN DR TRANSFAC: T00056; -
RN DR SGD: S0001595; ABE1.
RN KW Transcription regulation; Activator; DNA-binding; Nuclear protein;
RN KW Phosphorylation; Zinc-finger; Metal-binding; Zinc; DNA replication;
RN KW Trans-acting factor.
RN FT ZN_FING 49 71
RN FT MOD_RES 624 624
RN FT MUTAGEN 57 57
RN FT MUTAGEN 71 71
RN FT CONFLICT 125 125
RN FT CONFLICT 128 128
RN FT CONFLICT 148 148
RN FT CONFLICT 279 280
RN FT CONFLICT 690 690
RN FT SEQUENCE 731 AA; 81749 MW; BF200372P3A5EA5F CRC64;
RN
RN Query Match 45.3%; Score 43.5; DB 1; Length 731;
RN Best Local Similarity 50.0%; Pred. No. 51;
RN Matches 9; Conservative 3; Mismatches 5; Indels 1; Gaps 1;
RN
RN QY 1 NEREDERT-LTRKEYEDIV 17
RN ||:|:|:|:|:|
RN DB 221 NEEDDVHTQMTKNYSADV 238

```

DIP2\_YEAST  
ID DIP2\_YEAST STANDARD: PRT: 943 AA.  
AC Q12220: Q05386;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE DOM34 INTERACTING PROTEIN 2.  
GN DIP2 OR YLR129W OR U9233.1 OR L3116.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-S288C / AB972;  
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,  
RA Faveille A., Fulton L., Gattung S., Greco T., Kirschen J., Kucaba T.,  
RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,  
RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,  
RA Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,  
RA Tach A., Trevasakis E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,  
RA Wilson R., Waterston R.;  
RL Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-S288C;  
RA Delius H.;  
RL Submitted (JUN-1995) to the EMBL/Genbank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 1-458 FROM N.A.  
RC STRAIN-FY23 / RD005;  
RA Verhasselt P., Voet M., Volckaert G.;  
RL Submitted (MAY-1996) to the EMBL/Genbank/DBJ databases.  
CC -1- SIMILARITY: CONTAINS 10 WD REPEATS (TRP-ASP DOMAINS).  
CC -1- SIMILARITY: TO S.POMBE SPEC3D5.12.  
CC -----  
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CC -----  
DR EMBL: U53877.1; AAB82375.1; -;  
DR EMBL: U53881.1; AAB82402.1; -;  
DR EMBL: X91258.1; CAA62640.1; -;  
DR EMBL: Z73301.1; CAA97699.1; -;  
DR EMBL: Z73302.1; CAA97700.1; -;  
DR EMBL: X89514.1; CAA61707.1; -;  
DR SGD: S0004119.1; DIP2.  
DR InterPro: IPR001680; WD40.  
DR Pfam: PF00400; WD40.12.  
DR PRINTS: PR00320; GPROTEINRPT.  
DR SMART: SM00320; WD40.11.  
DR PROSITE: PS00678; WD\_REPEATS\_1; 4.  
DR PROSITE: PS00682; WD\_REPEATS\_2; 8.  
DR PROSITE: PS00294; WD\_REPEATS\_REGION; 1.  
KW Repeat; WD repeat.  
FT REPEAT 77 107 WD 1.  
FT REPEAT 119 149 WD 2.  
FT REPEAT 161 190 WD 3.  
FT REPEAT 202 230 WD 4.  
FT REPEAT 389 418 WD 5.  
FT REPEAT 428 458 WD 6.  
FT REPEAT 471 501 WD 7.  
FT REPEAT 571 601 WD 8.  
FT REPEAT 613 643 WD 9.  
FT REPEAT 655 685 WD 10.  
SQ SEQUENCE 943 AA: 106342 MW: 7D9AECTAFA6A9C740 CRC64;

Query Match

44.8%; Score 43; DB 1; Length 943;

Best Local Similarity 47.1%; Pred. No. 80;  
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 2 EREDERTLTKEVEDIVL 18  
DB 694 EEEKERLEEEQVEDIVL 710  
RESULT 15  
ID RL4\_MYCCA STANDARD: PRT: 208 AA.  
AC P10135;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 01-AUG-1992 (Rel. 23, Last annotation update)  
DE 50S RIBOSOMAL PROTEIN L4.  
GN RP.LD.  
OS Mycoplasma capricolum.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Molluscites;  
OC Entomoplasmataceae.  
OX NCBI\_TaxID=2095;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-ATCC 27343 / KID;  
RX MEDLINE=88142549; PubMed=3481422;  
RA Okubo S., Muto A., Kawauchi Y., Yamao F., Osawa S.;  
RT "The ribosomal protein gene cluster of Mycoplasma capricolum";  
RL Mol. Gen. Genet. 210:314-322(1987).  
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY AND SPECIFICALLY TO 23S  
CC RNA (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE L4P FAMILY OF RIBOSOMAL PROTEINS.  
CC -----  
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CC -----  
DR EMBL: X06414.1; CAA29705.1; -;  
DR PIR: S02832; R5YMAC.  
DR InterPro: IPR002136; Ribosomal\_L4/L1E.  
DR Pfam: PF00573; Ribosomal\_L4.1.  
KW Ribosomal protein; rRNA-binding.  
SQ SEQUENCE 208 AA: 23109 MW: D6D3BCDA541CB73A CRC64;

Query Match 43.8%; Score 42; DB 1; Length 208;  
Best Local Similarity 50.0%; Pred. No. 22;  
Matches 9; Conservative 6; Mismatches 1; Indels 2; Gaps 1;  
QY 4 EDERTL--TKEVEDIVK 19  
DB 149 DDQKTLTVKEKEELVVK 166

Search completed: January 29, 2002, 11:13:48  
Job time: 824 sec



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 11:12:14 ; Search time 285.36 Seconds  
(without alignments)  
9.739 Million cell updates/sec

Title: US-09-763-397A-20  
Perfect score: 96  
Sequence: 1 NEREDERTLTKEYEDIVLK 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues  
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_17.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	1433	5	Q9N9G9
2	96	100.0	1475	5	Q25842
3	89	92.7	1421	5	Q05644
4	89	92.7	1435	5	Q9NG63
5	50	52.1	368	10	Q9ZUX9
6	48	50.0	217	2	Q51118
7	48	50.0	669	2	Q9FC50
8	48	50.0	669	2	Q9FCR5
9	48	50.0	680	2	Q51283
10	48	50.0	685	2	Q9AKU7
11	48	50.0	689	2	Q51288
12	48	50.0	697	2	Q9EXC8
13	48	50.0	702	2	Q9FCR9
14	48	50.0	707	2	Q9EXB0
15	48	50.0	722	2	Q9AKU8
16	47	49.0	517	10	Q9XFJ4
17	46	47.9	213	12	O57212
18	46	47.9	384	10	Q9SIT3
19	46	47.9	409	10	Q9LV54

20	46	47.9	567	5	Q9NLC9
21	46	47.9	571	5	Q9NLD0
22	46	47.9	860	3	P87295
23	46	47.9	8243	5	O96554
24	45	46.9	256	10	Q08333
25	44.5	46.4	168	10	P82403
26	44.5	46.4	361	1	O57936
27	44	45.8	24	2	Q9R5S2
28	44	45.8	517	10	Q9S792
29	44	45.8	978	2	Q9PNK9
30	43	44.8	234	10	Q9LIQ6
31	43	44.8	268	2	O69068
32	43	44.8	319	2	Q9JYJ3
33	43	44.8	342	2	Q9PHT9
34	43	44.8	553	10	Q9AV84
35	43	44.8	585	5	Q9U4F0
36	43	44.8	601	10	Q9S7A8
37	43	44.8	695	2	Q9FCR8
38	43	44.8	698	2	Q9JPL7
39	43	44.8	702	4	Q9P2M4
40	43	44.8	715	2	Q9AKU6
41	43	44.8	990	5	Q9U4F1
42	43	44.8	1020	5	Q9U1K1
43	43	44.8	1337	5	Q9Y008
44	43	44.8	1342	5	O97364
45	43	44.8	1829	5	Q22248

#### ALIGNMENTS

RESULT 1  
Q9N9G9 ID Q9N9G9 PRELIMINARY: PRT; 1433 AA.  
AC Q9N9G9  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE ERYTHROCYTE BINDING PROTEIN (FRAGMENT).  
GN EBP.  
OS Plasmodium reichenowi.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5854;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CONGOLESE;  
RA Ozwara H., Kocken C.H.M., Thomas A.W.;  
RT "Molecular characterization of erythrocyte binding protein of  
RT Chimpanzee malaria parasite plasmodium reichenowi.";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ251848; CAB96159.1;  
DR InterPro: IPR001596; Pyrophosphatase.  
DR PROSITE: PS00387; PPASE; UNKNOWN\_1.  
FT NON\_TER 1  
FT CHAIN 9 >1433 ERYTHROCYTE BINDING PROTEIN.  
FT NON\_TER 1433 1433  
SQ SEQUENCE 1433 AA; 166648 MW; 733D0CDB6EDC27AE CRC64;

Query Match 100.0%; Score 96; DB 5; Length 1433;  
Best Local Similarity 100.0%; Pred. No. 1.7e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NEREDERTLTKEYEDIVLK 19  
|||||  
Db 1083 NEREDERTLTKEYEDIVLK 1101

RESULT 2  
Q25842 ID Q25842 PRELIMINARY: PRT; 1475 AA.  
AC Q25842;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)

Q9nlc9 caenorhabdi  
Q9nld0 caenorhabdi  
P87295 schizosacch  
O96554 cryptospori  
Q08333 zea mays (m  
P82403 spinacia ol  
O57936 pyrococcus  
Q9r5s2 lactobacill  
O9s792 nicotiana t  
O9pnk9 campylobact  
Q9liq6 arabidopsi  
O69068 pseudomonas  
Q9jy33 neisseria m  
Q9pht9 campylobact  
Q9av84 oryza sativ  
Q9u4f0 drosophila  
Q9s7a8 arabidopsi  
Q9fcr8 neisseria m  
Q9jpl7 neisseria m  
Q9p2m4 homo sapien  
Q9aku6 neisseria m  
Q9u4f1 drosophila  
Q9u1k1 drosophila  
Q9y008 plasmodium  
O97364 plasmodium  
Q22248 caenorhabdi

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DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE ERYTHROCYTE BINDING ANTIGEN 175.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92357776; PubMed=1496004;
RA Adams J.H., Sim B.K., Dolan S.A., Fang X., Kaslow D.C., Miller L.H.;
RT "A family of erythrocyte binding proteins of malaria parasites.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:7085-7089(1992).
DR EMBL; M93397; AAA29600.1; -.
SQ SEQUENCE 1475 AA; 171487 MW; EB8312823AFF946D CRC64;

Query Match 100.0%; Score 96; DB 5; Length 1475;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NEREDERTLTKEYEDIVLK 19
    |||||
Db 1069 NEREDERTLTKEYEDIVLK 1087

RESULT 3
Q05644 PRELIMINARY; PRT; 1421 AA.
AC Q05644;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ERYTHROCYTE BINDING ANTIGEN (EBA-175) (FRAGMENT).
GN EBA-175.
OS Plasmodium falciparum (isolate 3D7), and
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329, 5833;
RN [1]
RP SEQUENCE FROM N.A.
RX SPECIES=P. falciparum; STRAIN=ISOLATE 3D7;
RA Daugherty J.R., Lanar D.E.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 795-918 FROM N.A.
RX SPECIES=P. falciparum; STRAIN=ISOLATE FCR-3;
RX MEDLINE=93376008; PubMed=8366884;
RA Ware L.A., Kain K.C., Sim B.K., Haynes J.D., Baird J.K., Lanar D.E.;
RT "Two alleles of the 175-kilodalton Plasmodium falciparum erythrocyte
binding antigen.";
RL Mol. Biochem. Parasitol. 60:105-109(1993).
DR EMBL; U32207; AAA75179.1; -.
DR EMBL; L07755; AAA02927.1; -.
KW Antigen; Polymorphism.
FT NON_TER 1421
SQ SEQUENCE 1421 AA; 165330 MW; 7BE8DDFA07CEE771 CRC64;

Query Match 92.7%; Score 89; DB 5; Length 1421;
Best Local Similarity 94.7%; Pred. No. 0.00017;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NEREDERTLTKEYEDIVLK 19
    |||||
Db 1096 NEREDERTLTKEYEDIVLK 1114

RESULT 4
Q05644 PRELIMINARY; PRT; 1435 AA.
AC Q05644;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

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DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ERYTHROCYTE BINDING ANTIGEN 175.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=FCCL/HN;
RA Ma C.L., Yu X.B., Li X.R., Shan Z.X.;
RT "Conservation and antigenicity of erythrocyte binding antigen 175 in
Plasmodium falciparum isolate FCCL/HN.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF258781; AAF72186.1; -.
SQ SEQUENCE 1435 AA; 167269 MW; FE958828C7794F22 CRC64;

Query Match 92.7%; Score 89; DB 5; Length 1435;
Best Local Similarity 94.7%; Pred. No. 0.00018;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NEREDERTLTKEYEDIVLK 19
    |||||
Db 1069 NEREDERTLTKEYEDIVLK 1087

RESULT 5
Q05644 PRELIMINARY; PRT; 368 AA.
AC Q05644;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE F15K20.12 PROTEIN.
GN F15K20.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CV. COLOMBIA;
RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
RA Shen M., Renning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
RT "Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005824; AAC73022.1; -.
DR InterPro; IPR003617; TFS2_N.
DR SMART; SM00509; TFS2N; 2.
SQ SEQUENCE 368 AA; 42310 MW; 9834AC6A6C28E12 CRC64;

Query Match 52.1%; Score 50; DB 10; Length 368;
Best Local Similarity 56.2%; Pred. No. 18;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 NEREDERTLTKEYEDIVLK 16
    |||||
Db 170 NKKEQSLTRETETKI 185

RESULT 6
Q05118 PRELIMINARY; PRT; 217 AA.
AC Q05118;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE TRANSFERRIN BINDING PROTEIN 2 (FRAGMENT).
GN TBP2.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;

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Qy 2 EREDERTLTKEYEDIVLK 19
  || || : || : || :
Db 517 ERTDEKEIPKEQDIVR 534

RESULT 10
Q9AKU7 PRELIMINARY; PRT; 685 AA.
AC Q9AKU7; 2001 (TREMELREL. 17, Created)
DT 01-JUN-2001 (TREMELREL. 17, Last sequence update)
DT 01-JUN-2001 (TREMELREL. 17, Last annotation update)
DE TRANSFERRIN BINDING PROTEIN B.
GN TBPB.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=92/123;
RA Rokbi B.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y17806; CAC27780.1;
SQ SEQUENCE 685 AA; 73775 MW; 30ADB39EF34B31A5 CRC64;

Query Match 50.0%; Score 48; DB 2; Length 685;
Best Local Similarity 50.0%; Pred. No. 68;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 2 EREDERTLTKEYEDIVLK 19
  || || : || : || :
Db 522 ERTDEKEIPKEQDIVR 539

RESULT 11
Q51288 PRELIMINARY; PRT; 689 AA.
AC Q51288;
DT 01-NOV-1996 (TREMELREL. 01, Created)
DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)
DT 01-JUN-2001 (TREMELREL. 17, Last annotation update)
DE TRANSFERRIN-BINDING PROTEIN 2 PRECURSOR.
GN TBP2.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B283;
RA Legrain M.; Findeli A., Villevall D., Quentin-Millet M., Jacobs E.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50732; CAA90599.1;
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
KW Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 689 TRANSFERRIN-BINDING PROTEIN 2.
SQ SEQUENCE 689 AA; 74321 MW; 2D1D467569E6A722 CRC64;

Query Match 50.0%; Score 48; DB 2; Length 689;
Best Local Similarity 50.0%; Pred. No. 68;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 2 EREDERTLTKEYEDIVLK 19
  || || : || : || :
Db 526 ERTDEKEIPKEQDIVR 543

RESULT 12
Q9EXC8 PRELIMINARY; PRT; 697 AA.
ID Q9EXC8

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AC Q9EXC8;
DT 01-MAR-2001 (TREMELREL. 16, Created)
DT 01-MAR-2001 (TREMELREL. 16, Last sequence update)
DT 01-JUN-2001 (TREMELREL. 17, Last annotation update)
DE TRANSFERRIN BINDING PROTEIN B SUBUNIT (FRAGMENT).
GN TBPB.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z3905;
RA Achtman M., Ende A., Zhu P., Koroleva I.S., Kusecek B., Morelli G.,
RA Schuurman I.G.A., Brieske N., Zurth K., Kostyukova N.N.,
RA Platonov A.E.;
RT "Clonal groupings associated with successive waves of serogroup A
RT meningococcal disease from 1969 to 1997 in Moscow, Russia.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Z3905;
RA Zhu P., Ende A., Brieske N., Morelli G., Popovic T., Riou J.Y.,
RA Caugant D.A., Achtman M.;
RT "Microevolution in subgroup III Neisseria meningitidis during three
RT pandemics of epidemic meningitis.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Z3905;
RX MEDLINE=20305048; PubMed=10844690;
RA Linz B., Schenker M., Achtman M.;
RT "Frequent interspecific genetic exchange between commensal Neisseriae
RT and Neisseria meningitidis.";
RL Mol. Microbiol. 36:1049-1058(2000).
DR EMBL; AJ276915; CAC21580.1;
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
FT NON_TER 1
FT SEQUENCE 697 AA; 75846 MW; 3D577D2AC8DF129A CRC64;

Query Match 50.0%; Score 48; DB 2; Length 697;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 2 EREDERTLTKEYEDIVLK 19
  || || : || : || :
Db 538 ERTDEKEIPKEQDIVR 555

RESULT 13
Q9FCR9 PRELIMINARY; PRT; 702 AA.
ID Q9FCR9
AC Q9FCR9; 2001 (TREMELREL. 16, Created)
DT 01-MAR-2001 (TREMELREL. 16, Last sequence update)
DT 01-MAR-2001 (TREMELREL. 17, Last annotation update)
DE TRANSFERRIN BINDING PROTEIN B (FRAGMENT).
GN TBPB.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=92123;
RX MEDLINE=20407297; PubMed=10948108;
RA Rokbi B., Renauld-Mongenie G., Mignon M., Danve B., Poncet D.,
RA Chabanel C., Caugant D.A., Quentin-Millet M.J.;
RT "Allelic diversity of the two transferrin binding protein B Gene
RT isotypes among a collection of Neisseria Meningitidis strains
RT representative of serogroup b disease: implication for the composition
RT of a recombinant TbpB-based vaccine.";
RL Infect. Immun. 68:4938-4947(2000).

```



DR EMBL; AJ279558; CAC05592.1; -.  
 DR InterPro; IPR001677; Transferrin\_bind.  
 DR Pfam; PF01298; Lipoprotein\_5; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 702 AA; 75796 MW; 14DCB6B64DC13F75 CRC64;

Query Match 50.0%; Score 48; DB 2; Length 702;  
 Best Local Similarity 50.0%; Pred. No. 70;  
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 EREDERTLTKEYEDIVLK 19  
 || || : || : || :  
 Db 543 ERTDEKEIPKEQODIVYR 560

RESULT 14

Q9EXB0 PRELIMINARY; PRT; 707 AA.  
 AC Q9EXB0;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE TRANSFERRIN BINDING PROTEIN B SUBUNIT (FRAGMENT).  
 GN TBPB.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=24311;  
 RA Achtman M., Ende A., Zhu P., Koroleva I.S., Kusecek B., Morelli G.,  
 RA Schuurman I.G.A., Brieske N., Zurth K., Kostyukova N.N.,  
 RA Platonov A.E.;  
 RT "Clonal groupings associated with successive waves of serogroup A  
 meningococcal disease from 1969 to 1997 in Moscow, Russia."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=24311;  
 RA Zhu P., Ende A., Brieske N., Morelli G., Popovic T., Riou J.Y.,  
 RA Caugant D.A., Achtman M.;  
 RT "Microevolution in subgroup III Neisseria meningitidis during three  
 pandemics of epidemic meningitis."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=24311;  
 RX MEDLINE=20305048; PubMed=10844690;  
 RA Linz B., Schenker M., Achtman M.;  
 RT "Frequent interspecific genetic exchange between commensal neisseriae  
 and Neisseria meningitidis."  
 RL Mol. Microbiol. 36:1049-1058(2000).  
 DR EMBL; AJ276933; CAC21596.1; -.  
 DR InterPro; IPR001677; Transferrin\_bind.  
 DR Pfam; PF01298; Lipoprotein\_5; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 707 AA; 75729 MW; 9271A060B9DFED04 CRC64;

Query Match 50.0%; Score 48; DB 2; Length 707;  
 Best Local Similarity 50.0%; Pred. No. 70;  
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 EREDERTLTKEYEDIVLK 19  
 || || : || : || :  
 Db 542 ERTDEKEIPKEQODIVYR 559

RESULT 15

Q9AKU8 PRELIMINARY; PRT; 722 AA.  
 ID Q9AKU8  
 AC Q9AKU8;

DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE TRANSFERRIN BINDING PROTEIN B.  
 GN TBPB.  
 OS Neisseria meningitidis (serogroup B).  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=491;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=90/94;  
 RA Rokbi B.;  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Y17805; CAC27779.1; -.  
 SQ SEQUENCE 722 AA; 77921 MW; 0169743E83144B8D CRC64;

Query Match 50.0%; Score 48; DB 2; Length 722;  
 Best Local Similarity 50.0%; Pred. No. 72;  
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 EREDERTLTKEYEDIVLK 19  
 || || : || : || :  
 Db 563 ERTDEKEIPKEQODIVYR 580

Search completed: January 29, 2002, 11:12:15  
 Job time: 771 sec

us-09-763-397a-20.rspt

Mon Feb 4 15:23:43 2002

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 10:21:51 ; Search time 310.82 Seconds  
(without alignments)  
1.907 Million cell updates/sec

Title: US-09-763-397A-21  
Perfect score: 41  
Sequence: 1 LTPLEELY 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: /SID58/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID58/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
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4: /SID58/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID58/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID58/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SID58/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SID58/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SID58/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID58/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SID58/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SID58/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SID58/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
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21: /SID58/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	8	21	Plasmodium falcipa
2	41	100.0	9	18	Band-3 peptide SEQ
3	41	100.0	350	21	Recombinant vaccin
4	41	100.0	782	11	Polypeptide antige
5	39	95.1	123	21	Human secreted pro
6	39	95.1	447	12	smg p25A GDP Disso
7	36	87.8	92	21	Human secreted pro
8	36	87.8	284	22	Human colon cancer
9	34	82.9	283	20	Chlamydia trachoma
10	33	80.5	155	22	Human polypeptide
11	32	78.0	51	21	Arabidopsis thalia

12	32	78.0	52	21	AAG60903	Arabidopsis thalia
13	32	78.0	52	21	AAG61365	Arabidopsis thalia
14	32	78.0	76	22	AAM39585	Human polyptide
15	32	78.0	80	21	AAG59375	Arabidopsis thalia
16	32	78.0	81	21	AAG60029	Arabidopsis thalia
17	32	78.0	85	22	AAM41371	Human polyptide
18	32	78.0	89	21	AAG15329	Arabidopsis thalia
19	32	78.0	106	21	AAG57874	Arabidopsis thalia
20	32	78.0	106	21	AAG59661	Arabidopsis thalia
21	32	78.0	106	21	AAG59662	Arabidopsis thalia
22	32	78.0	108	21	AAG59374	Arabidopsis thalia
23	32	78.0	109	21	AAG60028	Arabidopsis thalia
24	32	78.0	113	21	AAG59373	Arabidopsis thalia
25	32	78.0	114	21	AAG60027	Arabidopsis thalia
26	32	78.0	117	21	AAG15328	Arabidopsis thalia
27	32	78.0	122	21	AAG15327	Arabidopsis thalia
28	32	78.0	134	21	AAG57873	Arabidopsis thalia
29	32	78.0	134	21	AAG59660	Arabidopsis thalia
30	32	78.0	134	21	AAG59961	Arabidopsis thalia
31	32	78.0	139	21	AAG57872	Arabidopsis thalia
32	32	78.0	139	21	AAG59659	Arabidopsis thalia
33	32	78.0	139	21	AAG59960	Arabidopsis thalia
34	32	78.0	414	20	AA34996	Chlamydia pneumoni
35	32	78.0	416	17	AAW06795	High osmolality GI
36	32	78.0	539	21	AAG36614	Arabidopsis thalia
37	32	78.0	556	21	AAG36613	Arabidopsis thalia
38	32	78.0	568	21	AAG36612	Arabidopsis thalia
39	31	75.6	75	18	AAW20395	H. pylori secreted
40	31	75.6	159	18	AAW20665	H. pylori secreted
41	31	75.6	271	21	AAW19619	Arabidopsis thalia
42	31	75.6	371	17	AAW83015	Human thyroid tran
43	31	75.6	371	22	AAU05583	Human Thyroid tran
44	31	75.6	2273	19	AAW70398	ATP binding casses
45	30	73.2	18	22	AAB98058	Human G4ST peptide

ALIGNMENTS

RESULT 1  
AAY70297  
ID AAY70297 standard; peptide; 8 AA.  
XX  
AC AAY70297;  
XX  
DT 06-JUN-2000 (first entry)  
XX  
DE Plasmodium falciparum RAP-1 antigenic epitope, p545.  
XX  
KW Recombinant protein; CDC/NIAID/VAC-1; multivalent; malaria; vaccine;  
KW T-cell epitope; tetanus toxoid; antigenic epitope; treatment;  
KW circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2;  
KW liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2;  
KW apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175;  
KW EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen;  
KW Pf27; antiparasitic; prevention; anti-CDC/NIAID/VAC-1 antibody.  
XX  
OS Plasmodium falciparum.

XX  
PN WO200011179-A1.  
XX  
PD 02-MAR-2000.  
XX  
PF 19-AUG-1999; 99WO-US18869.  
XX  
PR 21-AUG-1998; 98US-0097703.  
XX  
PA (NAIM-) NAT INST IMMUNOLOGY.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Lal AA, Shi YP, Hasnain SE;  
XX  
DR WPI; 2000-237654/20.

XX Novel recombinant protein as vaccine for treating malarial infection  
PT comprises antigenic peptides obtained from different stages of  
XX plasmodium falciparum life cycle  
XX  
XX Claim 2; Page 17; 52pp; English.  
XX  
XX The present sequence is the antigenic epitope P545, derived from  
CC rhoptry associated protein-1 (RAP-1) of the asexual blood stage of  
CC Plasmodium falciparum. It is used in the construction of recombinant  
CC protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial  
CC vaccine. The recombinant protein comprises, melittin signal peptide,  
CC (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes  
CC from circumsporozoite protein (CSP), sporozoite surface protein-2  
CC (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1  
CC (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding  
CC antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete  
CC specific antigen, Pf27. These epitopes were obtained at different stages  
CC of the life cycle of P. falciparum. CDC/NIIMALVAC-1 vaccine has  
CC antiparasitic activity and can be used for treatment and prevention of  
CC malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for  
CC detecting P. falciparum in biological samples.

SQ Sequence 8 AA;

Query Match 100.0%; Score 41; DB 21; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTPLEELY 8  
DB 1 ltpleely 8

RESULT 2

AAW35494  
ID AAW35494 standard; peptide; 9 AA.

XX AAW35494;

XX 22-APR-1998 (first entry)

XX Band-3 peptide SEQ ID NO:22 from WO9738011.

XX T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;  
KW scaffold; inhibition; metastasis; wound healing; solid phase.

XX Unidentified.

XX WO9738011-A1.

XX 16-OCT-1997.

XX 03-APR-1997; 97WO-DE00146.

XX 03-APR-1996; 96DK-0000398.

XX (PEPR-) PEPRESEARCH AS.

XX Heegaard PMH, Jakobsen PH;

XX WPI; 1997-512645/47.

XX Non-dendritic peptide carrier linked to a solid phase - useful as a  
PT diagnostic agent and as a scaffold for production of chemical  
PT derivatives

XX Example 5; Page 92; 262pp; English.

XX A non-dendritic peptide carrier (A) has been developed which is coupled  
CC through a linker to a solid phase, forming a complex of (A)-solid phase.  
CC Where (A) comprises 10-50 amino acids capable of forming a secondary

CC

CC structure in a benign buffer after liberation from the solid phase, and  
CC further the (A)-solid phase complex comprises an immunogenic substance  
CC and/or an immune mediator coupled on (A). The present sequence  
CC represents a peptide used in an example for the present invention. An  
CC (A)-solid phase complex can be used as a scaffold for the production of  
CC chemical derivatives, characterised by covalently attaching molecules at  
CC attachment points. Alternatively (A) is used as a scaffold-peptide for  
CC the incorporation into an immunostimulating complex (iscom) resulting an  
CC (A)-iscom complex which is used for the chemical coupling of antigenic  
CC substances in an aqueous solution by conjugation. (A) derivatised with  
CC one or more peptides having fibronectin-, laminin- or vitronectin-like  
CC binding activities can be used for the promotion of cell-attachment to  
CC plastic surfaces, in particular to inhibit tumour growth and metastasis,  
CC and for promotion of wound healing. Also a derivatised (A) can be used  
CC for the selection of specifically-binding aptamers or as a diagnostic  
CC agent. Such diagnostic (A) molecules could be used to detect molecules  
CC derived from or indicative of pregnancy or of a disease, such as an  
CC infectious, autoimmune or cancerous disease.

SQ Sequence 9 AA;

Query Match 100.0%; Score 41; DB 18; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTPLEELY 8  
DB 1 ltpleely 8

RESULT 3

AAW70278  
ID AAW70278 standard; Protein; 350 AA.

XX AAW70278;

XX 06-JUN-2000 (first entry)

XX Recombinant vaccine CDC/NIIMALVAC-1.

XX Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine;  
KW T-cell epitope; tetanus toxoid; antigenic epitope; treatment;  
KW circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2;  
KW liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2;  
KW apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175;  
KW EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen;  
KW Pf27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody;  
KW honey bee.

XX Chimeric - Apis sp.

XX Chimeric - Clostridium tetani.

XX Chimeric - Plasmodium falciparum.

XX Key Location/Qualifiers

XX Peptide 1..22 /label= Melittin\_signal\_peptide

XX FT /note= "Derived from Honey bee"

XX FT 23..350

XX Protein /label= Mature\_CDC/NIIMALVAC-1

XX FT /note= "Recombinant multivalent malarial vaccine"

XX WO200011179-A1.

XX 02-MAR-2000.

XX 19-AUG-1999; 99WO-US18869.

XX 21-AUG-1998; 98US-0097703.

XX (NALM-) NAT INST IMMUNOLOGY.  
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Lal AA, Shi YP, Hasnain SE;  
 XX WPI: 2000-237654/20.  
 DR N-PSDB; AAZ51336.  
 XX  
 PT Novel recombinant protein as vaccine for treating malarial infection  
 PT comprises antigenic peptides obtained from different stages of  
 PT plasmodium falciparum life cycle -  
 XX  
 PS Claim 3; Page 43-44; 52pp; English.  
 XX  
 CC The present sequence is that of recombinant protein CDC/NIIMALVAC-1,  
 CC which is a multivalent, multistage malarial vaccine. The recombinant  
 CC protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope  
 CC from tetanus toxoid and 21 antigenic epitopes from circumsporozoite  
 CC protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage  
 CC antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical  
 CC membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175),  
 CC rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pf27.  
 CC These epitopes were obtained at different stages of the life cycle of  
 CC Plasmodium falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic  
 CC activity and can be used for treatment and prevention of malarial  
 CC infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting  
 CC P. falciparum in biological samples.  
 XX  
 SQ Sequence 350 AA;  
 Query Match 100.0%; Score 41; DB 21; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LTPLEELY 8  
 Db 176 ltpleely 183  
 |||||  
 RESULT 4  
 AAR06991  
 ID AAR06991 standard; protein; 782 AA.  
 XX  
 AC AAR06991;  
 XX  
 DT 16-JAN-1991 (first entry)  
 XX  
 DE Polypeptide antigenic to rhoptry organelles of Plasmodium.  
 XX  
 KW Malaria; vaccine; rhoptry organelles.  
 XX  
 OS Plasmodium falciparum.  
 XX  
 PN EP388738-A.  
 XX  
 PD 26-SEP-1990.  
 XX  
 PF 09-MAR-1990; 90EP-0104561.  
 XX  
 PR 22-AUG-1989; 89GB-0019064.  
 PR 14-MAR-1989; 89GB-0005857.  
 XX  
 PA (HOFF ) HOFFMANN-LA ROCHE AG.  
 XX  
 PI Ridley RG, Scaife JG;  
 XX  
 DR WPI: 1990-291721/39.  
 DR N-PSDB; AAQ06000.  
 XX  
 PT Antigenic polypeptide and DNA encoding it - having a determinant  
 PT cross reactive with those on the rhoptry organelles of the  
 PT merozoite form of the malaria parasite P falciparum.  
 XX  
 PS Claim 1; Fig 2a-b; 29pp; English.  
 XX

CC Gene product may be isolated from a transformed E.coli (Y1088)  
 CC expression system using plasmid pMC9, and may then be used for  
 CC immunisation against malaria. The product may also be used  
 CC diagnostically to detect Abs directed against the parasite.  
 XX  
 SQ Sequence 782 AA;  
 Query Match 100.0%; Score 41; DB 11; Length 782;  
 Best Local Similarity 100.0%; Pred. No. 7.2;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LTPLEELY 8  
 Db 202 ltpleely 209  
 |||||  
 RESULT 5  
 AAG00310  
 ID AAG00310 standard; Protein; 123 AA.  
 XX  
 AC AAG00310;  
 XX  
 DT 06-OCT-2000 (first entry)  
 XX  
 DE Human secreted protein, SEQ ID NO: 4391.  
 XX  
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 KW gene therapy; chromosome mapping.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1033401-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PF 21-FEB-2000; 2000EP-0200610.  
 XX  
 PR 26-FEB-1999; 99US-0122487.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Dumas Milne Edwards J, Duclert A, Giordano J;  
 XX  
 DR WPI: 2000-500381/45.  
 DR N-PSDB; AAC00316.  
 XX  
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
 XX  
 PS Claim 13; SEQ ID 4391; 71pp + CD-ROM; English.  
 XX  
 CC The present sequence is a polypeptide encoded by one of a large number  
 CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs  
 CC were prepared from total human RNAs or polyA+ RNAs derived from 30  
 CC different tissues. EST sequences usually correspond mainly to the 3'  
 CC untranslated region (UTR) of the mRNA because they are often obtained  
 CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for  
 CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in  
 CC those cases where longer cDNA sequences have been obtained, the full 5'  
 CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'  
 CC ends and can therefore be used to obtain full length cDNAs and genomic  
 CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and  
 CC chromosome mapping procedures. They are used to obtain upstream  
 CC regulatory sequences and to design expression and secretion vectors.  
 XX  
 SQ Sequence 123 AA;  
 Query Match 95.1%; Score 39; DB 21; Length 123;  
 Best Local Similarity 87.5%; Pred. No. 2.5;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

PR	XX	26-FEB-1999;	99US-0122487.
XX	XX	(GEST ) GENSET.	
PA	XX	Dumas Milne Edwards J, Duclert A, Giordano J;	
PI	XX		
PT	XX	WPI; 2000-500381/45.	
PP	XX	N-PSDB; AAC00246.	
DR	XX	New nucleic acid that is a 5' expressed sequence tag (5' EST) for	
DT	XX	obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for	
DE	XX	diagnostic, forensic, gene therapy and chromosome mapping procedures -	
KW	XX	Claim 13; SEQ ID 4321; 71pp + CD-ROM; English.	
KN	XX	The present sequence is a polypeptide encoded by one of a large number	
PN	XX	of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs	
PD	CC	were prepared from total human RNAs or polyA+ RNAs derived from 30	
PF	CC	different tissues. EST sequences usually correspond mainly to the 3'	
PG	CC	untranslated region (UTR) of the mRNA because they are often obtained	
PH	CC	from oligo-dT primed cDNA libraries. Such ESTs are not well suited for	
PI	CC	isolating cDNA sequences derived from the 5' ends of mRNAs and even in	
PJ	CC	those cases where longer cDNA sequences have been obtained, intact 5'	
PK	CC	UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'	
PL	CC	ends and can therefore be used to obtain full length cDNAs and genomic	
PM	CC	DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and	
PN	CC	chromosome mapping procedures. They are used to obtain upstream	
PO	CC	regulatory sequences and to design expression and secretion vectors.	
PP	XX	Sequence 92 AA;	
PT	XX	Query Match 87.8%; Score 36; DB 21; Length 92;	
PU	XX	Best Local Similarity 75.0%; Pred. No. 7.2;	
PV	XX	Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	
QY	1	LTPLEELY 8	
DB	46	itpleely 53	
		:     :	
RESULT	8		
AAG73892	ID	AAG73892 standard; Protein; 284 AA.	
XX	AC	AAG73892;	
XX	DI	03-SEP-2001 (first entry)	
XX	DE	Human colon cancer antigen protein SEQ ID NO:4656.	
XX	DE	Human; colon cancer; colon cancer antigen; diagnosis; detection;	
XX	KW	colorectal carcinoma; chromosome 2.	
XX	OS	Homo sapiens.	
XX	PN	WO200122920-A2.	
XX	PD	05-APR-2001.	
XX	PF	28-SEP-2000; 2000WO-US26524.	
XX	PR	29-SEP-1999; 99US-0157137.	
XX	PR	03-NOV-1999; 99US-0163280.	
XX	PA	(HUMA-) HUMAN GENOME SCI INC.	
XX	PI	Ruben SM, Barash SC, Birse CE, Rosen CA;	
XX	PI	WPI; 2001-235357/24.	
XX	DR	N-PSDB; AAH33323.	
XX	PI	Nucleic acids encoding 4277 human colon cancer-associated polypeptides,	
XX	PI		

QY	1	LTPLEELY 8	
DB	46	itpleely 53	
		:     :	
RESULT	6		
AAR12388	ID	AAR12388 standard; Protein; 447 AA.	
XX	AC	AAR12388;	
XX	DT	29-AUG-1991 (first entry)	
XX	DE	sng p25A GDP Dissociation Inhibitory Protein.	
XX	DE	G-protein; Guanosine diphosphate; GDP; GDI.	
XX	KN	JF03113000-A.	
XX	PD	14-MAY-1991.	
XX	PF	26-SEP-1989; 89JP-0249441.	
XX	PR	26-SEP-1989; 89JP-0249441.	
XX	PA	(MITU ) MITSUBISHI KASEI CORP.	
XX	WT	WPI; 1991-183251/25.	
XX	DR	N-PSDB; AAQ11984.	
XX	PT	New protein for controlling levels of GTP-binding protein -	
XX	PT	using binding inhibition, by binding to G-protein to inhibit GDP	
XX	PT	GDP dissociation to GTP	
XX	PS	Claim 3; Page 1; 12pp; Japanese.	
XX	CC	The protein is a GDP Dissociation Inhibitory Protein (GDI) of mol.	
XX	CC	wt. 50-60kD which binds to low mol. wt. G-protein smg p25A.	
XX	XX	Sequence 447 AA;	
XX	QY	Query Match 95.1%; Score 39; DB 12; Length 447;	
XX	DB	Best Local Similarity 87.5%; Pred. No. 9.8;	
XX	DB	Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
XX	QY	1 LTPLEELY 8	
XX	DB	46 itpleely 53	
XX		:     :	
RESULT	7		
AAG00240	ID	AAG00240 standard; Protein; 92 AA.	
XX	AC	AAG00240;	
XX	DT	06-OCT-2000 (first entry)	
XX	DE	Human secreted protein, SEQ ID NO: 4321.	
XX	DE	Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;	
XX	KW	gene therapy; chromosome mapping.	
XX	OS	Homo sapiens.	
XX	PN	EP1033401-A2.	
XX	PD	06-SEP-2000.	
XX	PF	21-FEB-2000; 2000EP-0200610.	
XX	PI		

PT useful for preventing, diagnosing and/or treating colorectal cancers -  
 PS Claim 11; Page 6456-6458; 9803pp; English.  
 CC AAH32943 to AAH37195 and AAH73514 to AAH77788 represent human colon  
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where  
 CC the proteins are collectively known as colon cancer antigens. The colon  
 CC cancer antigens have cytostatic activity and can be used in gene  
 CC therapy and vaccine production. N and P may be used in the prevention,  
 CC diagnosis and treatment of diseases associated with inappropriate P  
 CC expression. For example, N and P may be used to treat disorders  
 CC associated with decreased expression by rectifying mutations or deletions  
 CC in a patient's genome that affect the activity of P by expressing  
 CC inactive proteins or to supplement the patients own production of P.  
 CC Additionally, N may be used to produce the colon cancer-associated Ps,  
 CC by inserting the nucleic acids into a host cell and culturing the cell  
 CC to express the proteins. N and P can be used in the prevention, diagnosis  
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204  
 CC and AAH77789 represent sequences used in the exemplification of the  
 CC present invention.  
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were  
 CC missing at time of publication, meaning no sequences are present for  
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.  
 XX  
 SQ Sequence 284 AA;

Query Match 87.8%; Score 36; DB 22; Length 284;  
 Best Local Similarity 75.0%; Pred. No. 24;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTPLEELY 8  
 :|||:|  
 DB 104 ltpledly 111

RESULT 9  
 AA36933  
 ID AA36933 standard; Protein; 283 AA.

AC AA36933;

DT 07-OCT-1999 (first entry)

DE Chlamydia trachomatis secreted protein.

KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;  
 KW paratrachoma; inclusion conjunctivitis; genital disease; perihhepatitis;  
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis;  
 KW bartholinitis; pneumopathy; venereal lymphogranulomatosis.

OS Chlamydia trachomatis.

XX WO9928475-A2.

PN 10-JUN-1999.

PD 27-NOV-1998; 98WO-IB01939.

PF 04-NOV-1998; 98US-0107077.

PR 28-NOV-1997; 97FR-0015041.

XX 17-DEC-1997; 97FR-0016034.

PA (GEST ) GENSET.

XX Griffiths R;

PI WPI; 1999-371125/31.

DR Genome sequence of Chlamydia trachomatis

PT Disclosure; Page 788-789; 1755pp; English.

XX

CC AA36754-Y37949 are encoded by open reading frames (ORFs) of the genome  
 CC of Chlamydia trachomatis (see AA201425). The polypeptides can be used as  
 CC vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences  
 CC can also be used to control growth of the microorganism. Chlamydia  
 CC trachomatis is responsible for a large number of diseases, e.g. eye  
 CC diseases such as conventional trachoma, nonendemic trachoma,  
 CC paratrachoma, and inclusion conjunctivitis; genital diseases such as  
 CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,  
 CC perihhepatitis, bartholinitis; pneumopathy in breast feeding infants;  
 CC and venereal lymphogranulomatosis. The polypeptides of the invention  
 CC may be of use in treating these diseases.

XX SQ Sequence 283 AA;

Query Match 82.9%; Score 34; DB 20; Length 283;  
 Best Local Similarity 75.0%; Pred. No. 59;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTPLEELY 8  
 :|||:|  
 DB 82 ltpienly 89

RESULT 10  
 AA39296  
 ID AA39296 standard; Protein; 155 AA.

AC AA39296;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 2441.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.

OS Homo sapiens.

XX WO200153312-A1.

PN 26-JUL-2001.

PD 26-DEC-2000; 2000WO-US34263.

PF 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

XX 29-NOV-2000; 2000US-0727344.

PA (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao QA, Zhou P, Goodrich R, Dmanac RT;

XX WPI; 2001-442253/47.

DR N-PSDB; AA158452.

XX Novel nucleic acids and polypeptides, useful for treating disorders  
 PT such as central nervous system injuries -

XX Example 4; SEQ ID NO 2441; 10078pp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and

the encoded polypeptides (AAM38642-AAM42213) with neurotropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed specification.

AA	Sequence	155 AA;
SO		

Query Match	80.5%;	Score 33;	DB 22;	Length 155;
Best Local Similarity	75.0%;	Pred. NO. 49;		
Matches	6:	Conservative	1; Mismatches	1; Indels 0; Gaps 0;

Qy 1 LTPLEELY 8  
1111:11  
Db 137 ltplqeay 144

RESULT 11  
AAG60904  
ID AAG60904 standard: Protein; 51 AA.

XX  
AC  
AAG60904:XX  
DT 18-OCT-2000 (first entry)

XX arabidopsis thaliana protein fragment SEQ ID NO: 78941.

protein identification; signal transduction pathway; metabolic pathway;  
hybridisation assay; genetic mapping; gene expression control; promoter;  
termination sequence.

XX Arabidopsis thaliana. 05

XX  
DN  
EP1033405-A2XX  
DD  
06-SEP-2000

XX 25-FEB-2000: 2000EP-0301439.

XX 99US-0121825.  
99US-1999.

PR 05-MAR-1999; 99US-0123180.  
00US-0123548

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126785.  
PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.  
 PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714  
10-APR-1000; 99US-0129845

19-APR-1999; 99US-0130077

PR 21-APR-1999; 99US-0130510  
PR 23-APR-1999; 99US-0130510

PR	23-APR-1999;	99US-0130051
PR	28-APR-1999;	99US-0131449

PR 30-APR-1999; 99US-0132407  
PR 30-APR-1999; 99US-0132407

PR	04-MAY-1999;	99US-0132484
22	05-MAY-1999;	99US-0132485

PR	06-MAY-1999;	99US-0132486
		99US-0132487

PR 07-MAY-1999; 99US-0132863

PR II-RAY-1999; 9903 VIS4200

PR	14-MAY-1999;	99US-0134218;
PR	14-MAY-1999;	99US-0134219;
PR	14-MAY-1999;	99US-0134221;
PR	14-MAY-1999;	99US-0134370;
PR	18-MAY-1999;	99US-0134376;
PR	19-MAY-1999;	99US-0134941;
PR	20-MAY-1999;	99US-0135124;
PR	21-MAY-1999;	99US-0135353;
PR	24-MAY-1999;	99US-0135629;
PR	25-MAY-1999;	99US-0136021;
PR	27-MAY-1999;	99US-0136392;
PR	28-MAY-1999;	99US-0136782;
PR	01-JUN-1999;	99US-0137222;
PR	01-JUN-1999;	99US-0137528;
PR	04-JUN-1999;	99US-0137502;
PR	07-JUN-1999;	99US-0137724;
PR	08-JUN-1999;	99US-0138094;
PR	10-JUN-1999;	99US-0138540;
PR	10-JUN-1999;	99US-0138847;
PR	14-JUN-1999;	99US-0139119;
PR	16-JUN-1999;	99US-0139439;
PR	17-JUN-1999;	99US-0139453;
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PR	18-JUN-1999;	99US-0139462;
PR	18-JUN-1999;	99US-0139463;
PR	18-JUN-1999;	99US-0139750;
PR	18-JUN-1999;	99US-0139763;
PR	18-JUN-1999;	99US-0139817;
PR	21-JUN-1999;	99US-0139899;
PR	22-JUN-1999;	99US-0140353;
PR	23-JUN-1999;	99US-0140354;
PR	24-JUN-1999;	99US-0140695;
PR	24-JUN-1999;	99US-0140823;
PR	28-JUN-1999;	99US-0140991;
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PR	01-JUL-1999;	99US-0142154;
PR	02-JUL-1999;	99US-0142055;
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PR	19-JUL-1999;	99US-0144335;
PR	20-JUL-1999;	99US-0144352;
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PR	21-JUL-1999;	99US-0145086;
PR	21-JUL-1999;	99US-0145088;
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PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
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PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
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PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
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PR 18-AUG-1999; 99US-0149426.
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PR 25-AUG-1999; 99US-0150566.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 24-SEP-1999; 99US-0155659.
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PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
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PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 78.0%; Score 32; DB 21; Length 51;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PLEELY 8
Db 34 pleely 39

RESULT 12
AAG60903
ID AAG60903 standard; Protein: 52 AA.
XX
AC AAG60903;
XX
XX 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 78939.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
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PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0123788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
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PR 18-MAY-1999; 99US-0134768.
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PR 20-MAY-1999; 99US-0135124.
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PR 21-MAY-1999;	99US-0135353.	PR 02-AUG-1999;	99US-0146388.
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Db 34 pleely 39
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 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
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 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.  
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 (HYSE-) HYSEQ INC.  
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 Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
 WPI: 2001-442253/47.  
 DR N-PSDB; AA158741.  
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 Novel nucleic acids and polypeptides, useful for treating disorders  
 such as central nervous system injuries -  
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 Example 4; SEQ ID NO 2730; 10078pp; English.  
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 The invention relates to human nucleic acids (AA157798-AA161369) and  
 the encoded polypeptides (AAM38642-AAM42213) with nootropic,  
 immunosuppressant and cytostatic activity. The polynucleotides are useful  
 in gene therapy. A composition containing a polypeptide or polynucleotide  
 of the invention may be used to treat diseases of the peripheral nervous  
 system, such as peripheral nervous injuries, peripheral neuropathy and  
 localised neuropathies and central nervous system diseases, such as  
 Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 utilisation of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
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 CC Note: The sequence data for this patent did not form part of the printed  
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XX  
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KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
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OS Arabidopsis thaliana.  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
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PF 25-FEB-2000; 2000EP-0301439.  
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PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.

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PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
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PR 18-OCT-1999; 99US-0159584.
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PR 22-OCT-1999; 99US-0160980.
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PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Job time: 428. sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 29, 2002, 10:24:11 ; Search time 133.18 seconds  
(without alignments)  
1.352 Million cell updates/sec

Title: US-09-763-397A-21  
Perfect score: 41  
Sequence: 1 LTPLEELY 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	Length			
1	31	75.6	371	2	US-08-442-809A-76	Sequence 76, Appl
2	30	73.2	1144	1	US-08-147-812-5	Sequence 5, Appl
3	30	73.2	1144	2	US-08-319-866-12	Sequence 12, Appl
4	30	73.2	1144	4	US-09-123-708-2	Sequence 2, Appl
5	30	73.2	1144	4	US-09-123-624-2	Sequence 2, Appl
6	30	73.2	1203	4	US-09-075-272-4	Sequence 4, Appl
7	30	73.2	3169	2	US-08-477-451-6	Sequence 6, Appl
8	29	70.7	102	3	US-08-946-329A-93	Sequence 93, Appl
9	29	70.7	251	2	US-08-665-647-7	Sequence 2, Appl
10	29	70.7	417	4	US-09-251-645-2	Sequence 2, Appl
11	29	70.7	480	4	US-09-078-173A-25	Sequence 25, Appl
12	29	70.7	480	4	US-09-537-357-32	Sequence 32, Appl
13	29	70.7	519	4	US-09-312-183A-3	Sequence 3, Appl
14	29	70.7	547	4	US-09-312-183A-2	Sequence 2, Appl
15	29	70.7	1976	3	US-09-024-020B-9	Sequence 9, Appl
16	29	70.7	1978	3	US-09-024-020B-3	Sequence 3, Appl
17	29	70.7	1988	3	US-09-024-020B-4	Sequence 4, Appl
18	28	68.3	9	1	US-08-139-054-7	Sequence 7, Appl
19	28	68.3	11	1	US-08-139-054-5	Sequence 5, Appl
20	28	68.3	11	1	US-08-139-054-9	Sequence 9, Appl
21	28	68.3	14	1	US-08-139-054-6	Sequence 6, Appl
22	28	68.3	142	4	US-08-945-983-7	Sequence 7, Appl
23	28	68.3	204	1	US-08-292-945-8	Sequence 8, Appl
24	28	68.3	204	1	US-08-252-073A-8	Sequence 8, Appl
25	28	68.3	204	5	PCT-US93-1207A-8	Sequence 8, Appl
26	28	68.3	340	2	US-08-578-592-5	Sequence 5, Appl
27	28	68.3	340	3	US-09-185-111-5	Sequence 5, Appl

28	28	68.3	342	4	US-09-461-474-16	Sequence 16, Appl
29	28	68.3	449	3	US-08-987-743-7	Sequence 7, Appl
30	28	68.3	462	2	US-08-477-451-24	Sequence 24, Appl
31	28	68.3	611	1	US-08-386-727-4	Sequence 4, Appl
32	28	68.3	611	2	US-08-600-452A-4	Sequence 4, Appl
33	28	68.3	863	2	US-08-666-271-2	Sequence 2, Appl
34	28	68.3	1079	2	US-08-929-967-8	Sequence 8, Appl
35	27	65.9	11	1	US-08-408-604A-32	Sequence 32, Appl
36	27	65.9	11	5	US-08-408-604A-43	Sequence 43, Appl
37	27	65.9	11	5	PCT-US93-09626-32	Sequence 32, Appl
38	27	65.9	11	5	PCT-US93-09626-43	Sequence 43, Appl
39	27	65.9	12	1	US-08-128-971B-11	Sequence 11, Appl
40	27	65.9	12	1	US-08-128-971B-14	Sequence 14, Appl
41	27	65.9	13	1	US-08-408-604A-36	Sequence 36, Appl
42	27	65.9	13	5	PCT-US93-09626-36	Sequence 36, Appl
43	27	65.9	18	4	US-08-652-877-39	Sequence 39, Appl
44	27	65.9	18	4	US-08-476-515A-39	Sequence 39, Appl
45	27	65.9	142	2	US-08-805-117-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1  
US-08-442-809A-76  
; Sequence 76, Application US/08442809A  
; Patent No. 5976873  
; GENERAL INFORMATION:  
; APPLICANT: Bohinski, Robert J.,  
; APPLICANT: Whitsett, Jeffrey A.  
; TITLE OF INVENTION: Nucleic Acid Sequences  
; TITLE OF INVENTION: Controlling Lung Cell -  
; TITLE OF INVENTION: Specific Gene Expression  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,  
; STREET: 6 Becker Farm Road  
; CITY: Roseland  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch diskette  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/442,809A  
; FILING DATE: 17-MAY-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/245,356  
; FILING DATE: 18-MAY-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Olstein, Elliot M.  
; REGISTRATION NUMBER: 24,025  
; REFERENCE/DOCKET NUMBER: 271010-360  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 76:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 371 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: human thyroid transcription factor-1  
; US-08-442-809A-76

us-09-763-397a-21.ra

Mon Feb 4 15:23:43 2002

TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
 STREET: Two Militia Drive  
 CITY: Lexington  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02173

QY 1 TPLEEL 8  
 Db 17 LSPLEEL 24

RESULT 2  
 US-08-147-812-5  
 ; Sequence 5, Application US/08147812  
 ; Patent No. 5766909  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xie, Qiao-wen  
 ; APPLICANT: Nathan, Carl F.  
 ; APPLICANT: Mumford, Richard A.  
 ; APPLICANT: Calaycay, Jimmy Ramos  
 ; TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Merck & Co., Inc.  
 ; STREET: 126 East Lincoln Avenue  
 ; CITY: Rahway  
 ; STATE: New Jersey  
 ; COUNTRY: USA  
 ; ZIP: 07065  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy Disk  
 ; COMPUTER: Macintosh Centris650  
 ; OPERATING SYSTEM: Macintosh 7.0.1  
 ; SOFTWARE: Microsoft Word 5.1a  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/147,812  
 ; FILING DATE: No. 5766909 Available  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/841,641  
 ; FILING DATE: 02-FEB-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Wallen, John W III  
 ; REGISTRATION NUMBER: 35,403  
 ; REFERENCE/DOCKET NUMBER: 186581A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (908) 594-3905  
 ; TELEFAX: (908) 594-4720  
 ; TELEX: 138825  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1144 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; US-08-147-812-5

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 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPLEEL 7  
 Db 128 TPLEEL 133

RESULT 3  
 US-08-319-866-12  
 ; Sequence 12, Application US/08319866  
 ; Patent No. 5923223  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tully, Timothy P.  
 ; APPLICANT: Yin, Jerry C.  
 ; APPLICANT: Regulski, Michael  
 ; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES

TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
 STREET: Two Militia Drive  
 CITY: Lexington  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02173  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/319,866  
 ; FILING DATE: 7-OCT-1994  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Granahan, Patricia  
 ; REGISTRATION NUMBER: 32,227  
 ; REFERENCE/DOCKET NUMBER: CSHL94-03  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617) 861-6240  
 ; TELEFAX: (617) 861-9540  
 ; INFORMATION FOR SEQ ID NO: 12:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1144 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-319-866-12

Query Match 73.2%; Score 30; DB 2; Length 1144;  
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 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPLEEL 7  
 Db 128 TPLEEL 133

RESULT 4  
 US-09-123-708-2  
 ; Sequence 2, Application US/09123708  
 ; Patent No. 6146887  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schraeder, Juergen  
 ; APPLICANT: GODECKE, Axel  
 ; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC  
 ; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS  
 ; FILE REFERENCE: 511169-2003  
 ; CURRENT APPLICATION NUMBER: US/09/123,708  
 ; CURRENT FILING DATE: 1998-07-28  
 ; EARLIER APPLICATION NUMBER: 08/553,503  
 ; EARLIER FILING DATE: 1996-03-01  
 ; EARLIER APPLICATION NUMBER: P4411402.8  
 ; EARLIER FILING DATE: 1994-03-31  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1144  
 ; TYPE: PRT  
 ; ORGANISM: Cytomegalovirus  
 ; US-09-123-708-2

Query Match 73.2%; Score 30; DB 4; Length 1144;  
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 Db 128 TPLEEL 133

Query Match 73.2%; Score 30; DB 4; Length 1144;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPLEEL 7  
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Db 128 TPLEEL 133

## RESULT 5

US-09-123-624-2  
; Sequence 2, Application US/09123624  
; Patent No. 6149936  
; GENERAL INFORMATION:  
; APPLICANT: SCHRADER, Jurgen  
; APPLICANT: CODECKE, Axel  
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC  
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS  
; FILE REFERENCE: 511169-2004  
; CURRENT APPLICATION NUMBER: US/09/123,624  
; CURRENT FILING DATE: 1998-07-28  
; PRIOR APPLICATION NUMBER: 08/553,503  
; PRIOR FILING DATE: 1996-03-01  
; PRIOR APPLICATION NUMBER: 4411402.8  
; PRIOR FILING DATE: 1994-03-31  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1144  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-123-624-2

Query Match 73.2%; Score 30; DB 4; Length 1144;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPLEEL 7  
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Db 128 TPLEEL 133

## RESULT 6

US-09-075-272-4  
; Sequence 4, Application US/09075272  
; Patent No. 6136598  
; GENERAL INFORMATION:  
; APPLICANT: MILLER, A. DUSTY  
; APPLICANT: WOLGAMOT, GREG  
; APPLICANT: BONHAM, LYNN  
; TITLE OF INVENTION: MUS DUNNI ENDOGENOUS RETROVIRAL  
; TITLE OF INVENTION: PACKAGING CELL LINES  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/075,272  
; FILING DATE: 08-MAY-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/046,140  
; FILING DATE: 09-MAY-1997  
; ATTORNEY/AGENT INFORMATION:

; NAME: Poor, Brian W.  
; REGISTRATION NUMBER: 32,928  
; REFERENCE/DOCKET NUMBER: 14538A-003710  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 467-9600  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1203 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-075-272-4

Query Match 73.2%; Score 30; DB 4; Length 1203;  
Best Local Similarity 75.0%; Pred. No. 7e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1035 LTPFEVLY 1042

## RESULT 7

US-08-477-451-6  
; Sequence 6, Application US/08477451  
; Patent No. 5928865  
; GENERAL INFORMATION:  
; APPLICANT: Covacci, Antonello  
; TITLE OF INVENTION: Helicobacter Pylori Cagi Region  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation  
; STREET: 4560 Horton Street  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,451  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McClung, Barbara G.  
; REGISTRATION NUMBER: 33,113  
; REFERENCE/DOCKET NUMBER: 0335.002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-601-2708  
; TELEFAX: 510-655-3542  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3169 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-477-451-6

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Best Local Similarity 85.7%; Pred. No. 2.1e+03;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTPLEEL 7  
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Db 2614 LSPLEEL 2620

us-09-763-397a-21.ra1

Mon Feb 4 15:23:43 2002

STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA: Patent Release #1.0, Version #1.30

APPLICATION NUMBER: US/08/665,647

FILING DATE: 18-JUN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 22550-20025.25

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 822-0168

TELEX: 90-4030 MRSNFORSWH

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 251 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-665-647-7

Query Match 70.7%; Score 29; DB 2; Length 251;

Best Local Similarity 62.5%; Pred. No. 1.9e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTPLEELY 8

Db 150 LDPKELY 157

RESULT 10

US-09-251-645-2

; Sequence 2, Application US/09251645

; Patent No. 6281413

; GENERAL INFORMATION:

; APPLICANT: Kramer, Vance C.

; APPLICANT: Morgan, Michael K.

; APPLICANT: Anderson, Arne R.

; APPLICANT: Hart, Hope

; APPLICANT: Warren, Gregory W.

; APPLICANT: Dunn, Martha

; APPLICANT: Chen, Jeng S.

; TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS

; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES CODING THEREFOR

; FILE REFERENCE: CGC1963/A

; CURRENT APPLICATION NUMBER: US/09/251,645

; CURRENT FILING DATE: 1999-02-17

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 417

; TYPE: PRT

; ORGANISM: Photorhabdus luminescens

US-09-251-645-2

Query Match 70.7%; Score 29; DB 4; Length 417;

Best Local Similarity 71.4%; Pred. No. 3.3e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TPLEELY 8

Db 311 TPLNDLY 317

RESULT 8

US-08-946-329A-93

; Sequence 93, Application US/08946329A

; Patent No. 6057091

; GENERAL INFORMATION:

; APPLICANT: Beachy, Philip A.

; APPLICANT: Porter, Jeffrey A.

; TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES

; NUMBER OF SEQUENCES: 109

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

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; STATE: CA

; COUNTRY: USA

; ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/946,329A

FILING DATE: 07-OCT-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/061,323

FILING DATE: 07-OCT-1996

APPLICATION NUMBER: 08/729,743

FILING DATE: 10-JUL-1996

APPLICATION NUMBER: 08/567,357

FILING DATE: 04-DEC-1995

APPLICATION NUMBER: 08/349,498

FILING DATE: 02-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Halle, Lisa A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/140001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5099

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INFORMATION FOR SEQ ID NO: 93:

SEQUENCE CHARACTERISTICS:

LENGTH: 102 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-946-329A-93

Query Match 70.7%; Score 29; DB 3; Length 102;

Best Local Similarity 62.5%; Pred. No. 69;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTPLEELY 8

Db 18 LITMEEMY 25

RESULT 9

US-08-665-647-7

; Sequence 7, Application US/08665647

; Patent No. 5935803

; GENERAL INFORMATION:

; APPLICANT: Desqueux, Nicki J.

; APPLICANT: Ron, Dorit

; APPLICANT: Voronova, Anna F.

; APPLICANT: Napolitano, Eugene W.

; TITLE OF INVENTION: METHODS TO IDENTIFY IMMUNOMODULATORS

; TITLE OF INVENTION: USING COGNATE INTERACTION OF PKC-THETA

; NUMBER OF SEQUENCES: 89

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FORSTER



us-09-763-397a-21.ra1

Mon Feb 4 15:23:43 2002

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,020B
; FILING DATE: 16-FEB-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,447
; FILING DATE: 26-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: CLARK, JANET P.
; REGISTRATION NUMBER: 34,799
; REFERENCE/DOCKET NUMBER: R0020B-REG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-3097
; TELEFAX: (650) 855-5322
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1976 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-024-020B-9

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Query Match          70.7%; Score 29; DB 3; Length 1976;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      3 PLEELY 8
Db     1029 PLDELY 1034

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Search completed: January 29, 2002, 10:24:12
Job time: 518 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 29, 2002, 10:26:47 ; Search time 144.96 Seconds  
(without alignments)  
4.204 Million cell updates/sec

Title: us-09-763-397a-21

Perfect score: 41

Sequence: 1 LTPLEELY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	782	2 S27833	rhopty-associated
2	39	95.1	447	2 I37082	GDP-dissociation i
3	39	95.1	447	2 A35652	smg p25A regulator
4	39	95.1	447	2 B56024	GDP dissociation i
5	39	95.1	447	2 A54091	rab GDP dissociati
6	38	92.7	444	2 T27222	hypothetical prote
7	36	87.8	445	2 A56024	GDP dissociation i
8	36	87.8	445	2 C56956	GDP dissociation i
9	36	87.8	445	2 B54091	rab GDP dissociati
10	35	85.4	448	2 S36746	GDP dissociation i
11	34	82.9	335	2 G83207	hypothetical prote
12	34	82.9	390	2 E72411	phosphopentomutase
13	34	82.9	412	2 D81693	conserved hypothet
14	34	82.9	414	2 B71538	probable hypotheti
15	34	82.9	990	2 T03784	probable receptor
16	33	80.5	117	2 A69828	hypothetical prote
17	33	80.5	139	2 T26722	hypothetical prote
18	33	80.5	338	2 S74042	probable pyruvate
19	33	80.5	393	2 B83841	phosphopentomutase
20	33	80.5	394	2 B69619	phosphodiesteribomu
21	33	80.5	609	2 A64432	modulation factor
22	33	80.5	632	2 S64786	hypothetical prote
23	32	78.0	139	2 T02564	hypothetical prote
24	32	78.0	139	2 H84729	hypothetical prote
25	32	78.0	304	2 A32108	translation initia
26	32	78.0	338	2 S38030	suppressor protein
27	32	78.0	366	2 G85699	glucokinase (EC 2.
28	32	78.0	366	2 E64866	hypothetical prote
29	32	78.0	386	2 S37691	ran GTPase activat

30	32	78.0	393	2 JE0180	phosphopentomutase
31	32	78.0	411	2 H72084	cbs domain protein
32	32	78.0	411	2 H86539	CBS domain protein
33	32	78.0	435	2 S64950	protein kinase HOG
34	32	78.0	514	2 S46733	hypothetical prote
35	32	78.0	532	2 S76525	methionine--tRNA I
36	32	78.0	532	2 T27457	hypothetical prote
37	32	78.0	602	2 T13219	major capsid prote
38	32	78.0	630	1 BWUT8Q	regulatory protein
39	32	78.0	630	2 A36359	VSG expression sit
40	32	78.0	630	2 S13724	ESAG 8 protein - T
41	32	78.0	848	2 C70203	DNA topoisomerase
42	32	78.0	1296	2 S55511	valine--tRNA ligas
43	31	75.6	133	2 T35218	hypothetical prote
44	31	75.6	157	2 G71843	probable dGTP pyro
45	31	75.6	295	2 E84425	probable homeodoma

#### ALIGNMENTS

##### RESULT 1

S27833  
rhopty-associated protein 1 precursor - malaria parasite (Plasmodium falciparum)  
N:Alternate names: protective antigen  
C:Species: Plasmodium falciparum  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jun-2000  
C:Accession: A45514; S27833  
R:Ridley, R.G.; Takacs, B.; Lahm, H.W.; Delves, C.J.; Goman, M.; Certa, U.; Matile, H.  
Mol. Biochem. Parasitol. 41, 125-134, 1990  
A:Title: Characterisation and sequence of a protective rhopty antigen from Plasmodiu  
A:Reference number: A45514; MUID:90348711  
A:Accession: A45514  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-782 <R12>  
A:Cross-references: GB:M32853; NID:gl60656; PID:gl60657  
C:Superfamily: Plasmodium falciparum rhopty-associated protein 1

Query Match 100.0%; Score 41; DB 2; Length 782;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTPLEELY 8  
Db 202 LTPLEELY 209

##### RESULT 2

I37082  
GDP-dissociation inhibitor XAP-4 - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 21-Jul-2000  
C:Accession: I37082; I39293  
R:Sedlacek, Z.; Konecki, D.S.; Korn, B.; Klauck, S.M.; Poustka, A.  
Mamm. Genome 5, 633-639, 1994  
A:Title: Evolutionary conservation and genomic organization of XAP-4, an Xq28 located  
A:Reference number: I37082; MUID:95152170  
A:Accession: I37082  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-447 <RE>  
A:Cross-references: EMBL:X79354; NID:9695522; PIDN:CAA55909.1; PID:9695523  
A:Accession: I39293  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-447 <RES>  
A:Cross-references: EMBL:X79353; NID:9695584; PID:9695585  
C:Genetics:  
A:Gene: GDB:RABGDIA  
A:Cross-references: GDB:I347097  
A:Introns: 15/3; 51/3; 85/1; 130/1; 196/2; 240/2; 273/3; 331/1; 379/2; 397/3

Mon Feb 4 15:23:43 2002

R:Nishimura, N.; Nakamura, H.; Takai, Y.; Sano, K.  
 J. Biol. Chem. 269, 14191-14198, 1994  
 A:Title: Molecular cloning and characterization of two rab GDI species from rat brain  
 A:Reference number: A54091; MUID:94245743  
 A:Accession: A54091  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-447 <NIS>  
 A:Cross-references: GB:X74402  
 R:Nishimura, N.  
 submitted to the EMBL Data Library, July 1993  
 A:Reference number: S35964  
 A:Accession: S35964  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-255, 'D', 257-288, 'D', 290-447 <NI2>  
 A:Cross-references: EMBL:X74402; NID:9396430; PIDN:CAA52413.1; PID:9396431  
 R:Ueda, T.; Takeyama, Y.; Ohmori, T.; Ohyanagi, H.; Saitoh, Y.; Takai, Y.  
 Biochemistry 30, 909-917, 1991  
 A:Title: Purification and characterization from rat liver cytosol of a GDP dissociati  
 SA GDI  
 A:Reference number: A37996; MUID:91113701  
 A:Accession: A37996  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 30-49; 104-112; 157-186; 270-285, 'T', 287-288, 'D', 290-293 <UED>  
 C:Superfamily: human GDP dissociation inhibitor XAP-4

Query Match 95.1%; Score 39; DB 2; Length 447;  
 Best Local Similarity 87.5%; Pred. No. 2.8;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LTPLEELY 8  
 Db 46 ITPLEELY 53

RESULT 6  
 T27222  
 hypothetical protein Y57G11C.10 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 26-May-2000  
 C:Accession: T27222  
 R:McMurray, A.  
 submitted to the EMBL Data Library, September 1997  
 A:Reference number: Z20330  
 A:Accession: T27222  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-444 <WIL>  
 A:Cross-references: EMBL:Z99281; PIDN:CAB16511.1; GSPDB:GN00022; CESP:Y57G11C.10  
 A:Experimental source: clone Y57G11C  
 C:Genetics:  
 A:Gene: CESP:Y57G11C.10  
 A:Map position: 4  
 A:Introns: 332/1; 416/3  
 C:Superfamily: human GDP dissociation inhibitor XAP-4

Query Match 92.7%; Score 38; DB 2; Length 444;  
 Best Local Similarity 87.5%; Pred. No. 4.5;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LTPLEELY 8  
 Db 46 ITPLEELY 53

RESULT 7  
 A56024  
 GDP dissociation inhibitor 2 - mouse  
 C:Species: Mus musculus (house mouse)

C:Superfamily: human GDP dissociation inhibitor XAP-4  
 Query Match 95.1%; Score 39; DB 2; Length 447;  
 Best Local Similarity 87.5%; Pred. No. 2.8;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LTPLEELY 8  
 Db 46 ITPLEELY 53  
 RESULT 3  
 A35652  
 smg p25A regulatory protein - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 28-Sep-1990 #sequence\_revision 28-Sep-1990 #text\_change 20-Jun-2000  
 C:Accession: A35652  
 R:Matsui, Y.; Kikuchi, A.; Araki, S.; Hata, Y.; Kondo, J.; Teranishi, Y.; Takai, Y.  
 Mol. Cell. Biol. 10, 4116-4122, 1990  
 A:Title: Molecular cloning and characterization of a novel type of regulatory protein (G  
 A:Reference number: A35652; MUID:90318376  
 A:Accession: A35652  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-447 <NAV>  
 A:Cross-references: GB:D90103; NID:q217563; PIDN:BAAL4134.1; PID:g217564; GB:M55560  
 C:Superfamily: human GDP dissociation inhibitor XAP-4

Query Match 95.1%; Score 39; DB 2; Length 447;  
 Best Local Similarity 87.5%; Pred. No. 2.8;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LTPLEELY 8  
 Db 46 ITPLEELY 53

RESULT 4  
 B56024  
 GDP dissociation inhibitor 1 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 26-May-2000  
 C:Accession: B56024  
 R:Shisheva, A.; Suedhof, T.C.; Czech, M.P.  
 Mol. Cell. Biol. 14, 3459-3468, 1994  
 A:Title: Cloning, characterization, and expression of a novel GDP dissociation inhibitor  
 A:Reference number: A56024; MUID:94217740  
 A:Accession: B56024  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-447 <SHI>  
 A:Cross-references: GB:U07952; NID:g493330; PIDN:AB16909.1; PID:g516540  
 C:Superfamily: human GDP dissociation inhibitor XAP-4

Query Match 95.1%; Score 39; DB 2; Length 447;  
 Best Local Similarity 87.5%; Pred. No. 2.8;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LTPLEELY 8  
 Db 46 ITPLEELY 53

RESULT 5  
 A54091  
 rab GDP dissociation inhibitor alpha - rat  
 N:Alternate names: rab GDI alpha  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 26-May-2000  
 C:Accession: A54091; S35964; A37996



C;Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 26-May-2000

C;Accession: A56024  
R;Shisheva, A.; Suedhof, T.C.; Czech, M.P.  
Mol. Cell. Biol. 14, 3459-3468, 1994  
A;Title: Cloning, characterization, and expression of a novel GDP dissociation inhibitor  
A;Reference number: A56024; MUID:94217740  
A;Accession: A56024  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-445 <SHI>  
A;Cross-references: GB:U07951  
C;Superfamily: human GDP dissociation inhibitor XAP-4

Query Match 87.8%; Score 36; DB 2; Length 445;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTPLEELY 8  
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Db 46 ITPLEDLY 53

## RESULT 8

C56956  
GDP dissociation inhibitor beta - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 26-May-2000  
C;Accession: C56956  
R;Janoueix-Lerosey, I.; Jollivet, P.; Camonis, J.; Marche, P.N.; Goud, B.  
J. Biol. Chem. 270, 14801-14808, 1995  
A;Title: Two-hybrid system screen with the small GTP-binding protein Rab6. Identification  
A;Reference number: A56956; MUID:95301579  
A;Accession: C56956  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-445 <JAN>  
A;Cross-references: GB:L36314; NID:g538410; PIDN:AAA78786.1; PID:g538411  
C;Superfamily: human GDP dissociation inhibitor XAP-4

Query Match 87.8%; Score 36; DB 2; Length 445;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTPLEELY 8  
:|||||:  
Db 46 ITPLEDLY 53

## RESULT 9

B54091  
rab GDP dissociation inhibitor beta - rat  
N;Alternate names: rab GDI beta  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 26-May-2000  
C;Accession: B54091; S35965  
R;Nishimura, N.; Nakamura, H.; Takai, Y.; Sano, K.  
J. Biol. Chem. 269, 14191-14198, 1994  
A;Title: Molecular cloning and characterization of two rab GDI species from rat brain: h  
A;Reference number: A54091; MUID:94245743  
A;Accession: B54091  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-445 <NIS>  
A;Cross-references: GB:X74401; NID:g396432; PIDN:CAA52412.1; PID:g396433  
R;Nishimura, N.  
submitted to the EMBL Data Library, July 1993

A;Reference number: S35964  
A;Accession: S35965  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-445 <NIS2>

A;Cross-references: EMBL:X74401; NID:g396432; PIDN:CAA52412.1; PID:g396433  
C;Superfamily: human GDP dissociation inhibitor XAP-4

Query Match 87.8%; Score 36; DB 2; Length 445;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTPLEELY 8  
:|||||:  
Db 46 ITPLEDLY 53

## RESULT 10

S36746  
GDP dissociation inhibitor - fruit fly (Drosophila melanogaster)  
C;Species: Drosophila melanogaster  
C;Date: 09-Dec-1993 #sequence\_revision 12-Apr-1996 #text\_change 26-May-2000  
C;Accession: S36746; S62097; S37806  
R;Zahner, J.E.; Cheney, C.M.  
Mol. Cell. Biol. 13, 217-227, 1993  
A;Title: A Drosophila homolog of bovine smg p25a GDP dissociation inhibitor undergoes  
A;Reference number: S36746; MUID:93109305  
A;Accession: S36746  
A;Molecule type: mRNA  
A;Residues: 1-448 <ZAH1>  
A;Cross-references: EMBL:L03209  
A;Accession: S62097  
A;Molecule type: protein  
A;Residues: 24-47;83-106; 'L', 230-248;353-383 <ZAH3>  
R;Zahner, J.E.; Cheney, C.M.  
submitted to the EMBL Data Library, March 1993  
A;Reference number: S37806  
A;Accession: S37806  
A;Molecule type: mRNA  
A;Residues: 1-124; 'RPWHP', 130-448 <ZAH2>  
A;Cross-references: EMBL:L03209; NID:g157491; PID:g157492  
C;Genetics:  
A;Gene: FlyBase:Gdi  
A;Cross-references: FlyBase:FBgn0004868  
C;Superfamily: human GDP dissociation inhibitor XAP-4

Query Match 85.4%; Score 35; DB 2; Length 448;  
Best Local Similarity 75.0%; Pred. No. 19;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTPLEELY 8  
:|||||:  
Db 47 ITPLEELF 54

## RESULT 11

G83207  
hypothetical protein PA3513 [imported] - Pseudomonas aeruginosa (strain PA01)  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C;Accession: G83207  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L  
; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa  
A;Reference number: A82950; MUID:20437337  
A;Accession: G83207  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-335 <STO>  
A;Cross-references: GB:AE004771; GB:AE004091; NID:g9949650; PIDN:AAG06901.1; GSPDB:GN  
C;Genetics:  
A;Gene: PA3513

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Query Match      82.9%; Score 34; DB 2; Length 335;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPLEELY 8
DB 311 TPLEELY 317

RESULT 12
E72411
Phosphopentomutase - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: E72411
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316
A:Accession: E72411
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-390 <ARN>
A:Cross-references: GB:AE001701; GB:AE000512; NID:g4980648; PIDN:AAD35260.1; PID:g498066
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0167
C:Superfamily: phosphopentomutase

Query Match      82.9%; Score 34; DB 2; Length 390;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 LTPLEELY 8
DB 163 IVPLEELY 170

RESULT 13
D81693
conserved hypothetical protein TC0527 [imported] - Chlamydia muridarum (strain Nigg)
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Jun-2000
C:Accession: D81693
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255
A:Accession: D81693
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-412 <TE>
A:Cross-references: GB:AE002321; GB:AE002160; NID:g7190560; PIDN:AAF39369.1; PID:g719056
A:Experimental source: strain Nigg (MoPn)
C:Genetics:
A:Gene: TC0527
C:Superfamily: hypothetical protein HI0107

Query Match      82.9%; Score 34; DB 2; Length 412;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 LTPLEELY 8
DB 213 LTPLEELY 220

RESULT 14
B71538
probable hypothetical protein containing cbs domains - Chlamydia trachomatis (serotyp
C:Species: Chlamydia trachomatis
C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 17-Mar-2000
C:Accession: B71538
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t
A:Reference number: A71570; MUID:99000809
A:Accession: B71538
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-414 <ARN>
A:Cross-references: GB:AE001298; GB:AE001273; NID:g3328659; PIDN:RAC67849.1; PID:g332
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: CT256
C:Superfamily: hypothetical protein HI0107

Query Match      82.9%; Score 34; DB 2; Length 414;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTPLEELY 8
DB 213 LTPLEELY 220

RESULT 15
T03784
probable receptor protein kinase - rice
C:Species: Oryza sativa (rice)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C:Accession: T03784
R:Xu, Y.; Zhu, Q.; Lamb, C.
submitted to the EMBL Data Library, June 1995
A:Description: Molecular cloning and characterization of a rice gene encoding leucine
A:Reference number: Z15083
A:Accession: T03784
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-990 <XUY>
A:Cross-references: EMBL:X89226; NID:gl263159; PIDN:CAA61510.1
A:Experimental source: cv. IR36, leaf
C:Genetics:
A:Gene: lrk2
A:Introns: 870/1
C:Superfamily: protein kinase Xa21; leucine-rich alpha-2-glycoprotein repeat homology

Query Match      82.9%; Score 34; DB 2; Length 990;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTPLEELY 8
DB 217 LTPLEELY 224

Search completed: January 29, 2002, 10:26:47
Job time: 658 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 29, 2002, 11:13:48 ; Search time 80.65 seconds  
(without alignments)  
3.637 Million cell updates/sec

Title: US-09-763-397A-21  
Perfect score: 41  
Sequence: 1 LTPLEELY 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	39	95.1	447	1 GDIA_BOVIN	P21856 bos taurus
2	39	95.1	447	1 GDIA_CANFA	O97555 canis famil
3	39	95.1	447	1 GDIA_HUMAN	P31150 homo sapien
4	39	95.1	447	1 GDIA_RAT	P50398 rattus norv
5	36	87.8	445	1 GDIB_CANFA	O97556 canis famil
6	36	87.8	445	1 GDIB_HUMAN	P50395 homo sapien
7	36	87.8	445	1 GDIB_MOUSE	P50397 mus musculu
8	36	87.8	445	1 GDIC_MOUSE	Q61598 mus musculu
9	36	87.8	445	1 GDIC_RAT	P50399 rattus norv
10	33	80.5	396	1 DBOB_BAGSU	P46353 bacillus su
11	33	80.5	609	1 YA58_METJA	O58458 methanococ
12	32	78.0	304	1 IF2A_YEAST	P20459 saccharomyc
13	32	78.0	368	1 SD22_YEAST	P36047 saccharomyc
14	32	78.0	366	1 YCGT_ECOLI	P76015 escherichia
15	32	78.0	386	1 RNAL_SCHPO	P41391 schizosacch
16	32	78.0	424	1 MR15_DROME	O9Y011 drosophila
17	32	78.0	435	1 HOG1_YEAST	P32485 saccharomyc
18	32	78.0	514	1 YHK8_YEAST	P38776 saccharomyc
19	32	78.0	532	1 SYM_SYNY3	Q55729 synecocyst
20	32	78.0	630	1 ESA8_TRYBO	P23799 trypanosoma
21	32	78.0	630	1 ESA8_TRYBO	P26337 trypanosoma
22	32	78.0	848	1 T0P1_BORBU	O51768 borrelia bu
23	31	75.6	157	1 NUDH_HELPJ	O92J28 helicobacte
24	31	75.6	371	1 TTF1_CANFA	P43698 canis famil
25	31	75.6	371	1 TTF1_HUMAN	P50220 mus musculu
26	31	75.6	372	1 TTF1_MOUSE	P50220 mus musculu
27	31	75.6	372	1 TTF1_RAT	P23441 rattus norv
28	31	75.6	578	1 P5P2_YEAST	P50109 saccharomyc
29	31	75.6	583	1 YCV1_YEAST	P25639 saccharomyc
30	31	75.6	1046	1 POL_FENV1	P31792 feline endo
31	31	75.6	2273	1 ABCR_HUMAN	P78363 homo sapien
32	30	73.2	105	1 GLN1_METBA	P54808 methanosarc
33	30	73.2	132	1 Y947_ARCFU	O29315 archaeoglob

ALIGNMENTS				
RESULT	1			
GDIA_BOVIN	34	73.2	169	1 MEMG_METCA
ID GDIA_BOVIN	35	30	73.2	1 Y226_AQUAE
AC P21856:	36	30	73.2	1 Y165_RICPR
DT 01-MAY-1991 (Rel. 18, Created)	37	30	73.2	1 HOG1_CANAL
DT 01-MAY-1991 (Rel. 18, Last sequence update)	38	30	73.2	1 SEDA_HELPJ
DT 15-JUL-1998 (Rel. 36, Last annotation update)	39	30	73.2	1 SEDA_HELPJ
DE RAB GDP DISSOCIATION INHIBITOR ALPHA (RAB GDI ALPHA) (GDI-1) (SMG P25A	40	30	73.2	1 N062_HUMAN
DE GDI).	41	30	73.2	1 DXS_ECOLI
GN GDI1 OR RABGDI1.	42	30	73.2	1 HUTH_HUMAN
OS Bos taurus (Bovine).	43	30	73.2	1 HUTH_MOUSE
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;	44	30	73.2	1 HUTH_RAT
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	45	30	73.2	1 HUTH_RAT
OC Bovidae; Bovinae; Bos.				
OX NCBI_TaxID=9913;				
RN [1]				
RP SEQUENCE FROM N.A.				
RX MEDLINE=90318376; PubMed=2115118;				
RA Matsui Y., Kikuchi A., Araki S., Hata Y., Kondo J., Teranishi Y.,				
RA Takai Y.;				
RT "Molecular cloning and characterization of a novel type of regulatory				
RT protein (GDI) for smg p25A, a ras p21-like GTP-binding protein.";				
RL Mol. Cell. Biol. 10:4115-4122(1990).				
RN [2]				
RP SIMILARITY TO CHOROIDEAEMIA PROTEIN.				
RX MEDLINE=91270365; PubMed=1904992;				
RA Fodor E., Lee R.T., O'Donnell J.J.;				
RT "Analysis of choroideaemia gene.";				
RL Nature 351:614-614(1991).				
RN [3]				
RP X-RAY CRYSTALLOGRAPHY (1.81 ANGSTROMS).				
RX MEDLINE=96196507; PubMed=8609986;				
RA Schalk I., Zeng K., Wu S.-K., Stura E.A., Matteson J., Huang M.,				
RA Tandon A., Wilson I.A., Balch W.E.;				
RT "Structure and mutational analysis of Rab GDP-dissociation				
RT inhibitor.";				
RL Nature 381:42-48(1996).				
CC -!- FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST RAB				
CC PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE				
CC SUBSEQUENT BINDING OF GTP TO THEM.				
CC -!- SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATION				
CC INHIBITOR.				
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CC -----				
DR EMBL; D90103; BAAL4134.1; -				
DR PIR; A35652; A35652.				
DR PDB; 1GND; 12-FEB-97.				
DR InterPro; IPR002005; Rab_GDI_REP.				
DR Pfam; PF00996; GDI; 1.				

DR PRINTS; PRO0891; RABGDIREP.  
DR PRINTS; PRO0892; RABGDI.  
KW GTPase activation; 3D-structure.  
SQ SEQUENCE 447 AA; 50565 MW; 69C68B03BDC1BA3F CRC64;  
  
Query Match 95.1%; Score 39; DB 1; Length 447;  
Best Local Similarity 87.5%; Pred. No. 0.82;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 LTPLEELY 8  
Db 46 ITPLEELY 53  
  
RESULT 2  
GDIA\_CANFA STANDARD; PRT; 447 AA.  
AC O9755;  
DT 20-AUG-2001 (Rel. 40, Created)  
DT 20-AUG-2001 (Rel. 40, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE RAB GDP DISSOCIATION INHIBITOR ALPHA (RAB GDI ALPHA) (GDI-1).  
GN GD1.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A. PubMed=9802909;  
RX MEDLINE=99019719; PubMed=9802909;  
RA Chen W., Feng Y., Chen D., Wandinger-Ness A.;  
RT "Rab11 is required for trans-golgi network-to-plasma membrane  
transport and a preferential target for GDP dissociation inhibitor.";  
RL Mol. Biol. Cell 9:3241-3257(1998).  
CC -1- FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST RAB  
CC PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE  
CC SUBSEQUENT BINDING OF GTP TO THEM.  
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATION  
CC INHIBITOR.  
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CC -----  
DR EMBL; AF027360; AAD04246.1; -.  
DR HSSP; P21856; 1GND.  
DR InterPro; IPR002005; Rab\_GDI\_REP.  
DR Pfam; PF00996; GDI\_1  
DR PRINTS; PRO0891; RABGDIREP.  
KW GTPase activation.  
SQ SEQUENCE 447 AA; 50520 MW; 10280DAD33E4BCD0 CRC64;  
  
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Best Local Similarity 87.5%; Pred. No. 0.82;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 LTPLEELY 8  
Db 46 ITPLEELY 53  
  
RESULT 3  
GDIA\_HUMAN STANDARD; PRT; 447 AA.  
ID GDIA\_HUMAN  
AC P31150; P50394;  
DT 01-JUL-1993 (Rel. 26, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE RAB GDP DISSOCIATION INHIBITOR ALPHA (RAB GDI ALPHA) (GDI-1) (XAP-4).  
GN GD11 OR RABGDIA OR XAP4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. PubMed=7849400;  
RX MEDLINE=95152170; PubMed=7849400;  
RA Sedlacek Z., Konecki D.S., Korn B., Klauck S.M., Poustka A.;  
RT "Evolutionary conservation and genomic organization of XAP-4, an Xq28  
RT located gene coding for a human rab GDP-dissociation inhibitor  
RT (GDI).";  
RL Mamm. Genome 5:633-639(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Retina;  
RX MEDLINE=96062207; PubMed=7595614;  
RA Nishimura N., Goji J., Nakamura H., Orita S., Takai Y., Sano K.;  
RT "Cloning of a brain-type isoform of human Rab GDI and its expression  
RT in human neuroblastoma cell lines and tumor specimens.";  
RL Cancer Res. 55:5445-5450(1995).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96311563; PubMed=8733135;  
RA Chen E.Y., Zollo M., Mazzarella R.A., Ciccodicola A., Chen C.-N.,  
RA Zuo L., Heiner C., Burrough F.W., Ripetto M., Schlessinger D.,  
RA D'Urso M.;  
RT "Long-range sequence analysis in Xq28: thirteen known and six  
RT candidate genes in 219.4 kb of high GC DNA between the RCP/GCP and  
RT G6PD loci.";  
RL Hum. Mol. Genet. 5:659-668(1996).  
RN [4]  
RP SEQUENCE OF 143-181 FROM N.A.  
RA Hochgeschwender U.;  
RT Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 328-436 FROM N.A.  
RA Bhat K.S.;  
RT Submitted (XXY-1992) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE OF 349-361.  
RX TISSUE=Keratinocytes;  
RX MEDLINE=93162043; PubMed=1286667;  
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,  
RA Vandekerckhove J.;  
RT "Microsequences of 145 proteins recorded in the two-dimensional gel  
RT protein database of normal human epidermal keratinocytes.";  
RL Electrophoresis 13:960-969(1992).  
RN [7]  
RP TISSUE SPECIFICITY.  
RX MEDLINE=95359978; PubMed=7543319;  
RA Bachner D., Sedlacek Z., Korn B., Hameister H., Poustka A.;  
RT "Expression patterns of two human genes coding for different rab GDP-  
RT dissociation inhibitors (GDIs), extremely conserved proteins involved  
RT in cellular transport.";  
RL Hum. Mol. Genet. 4:701-708(1995).  
RN [8]  
RP VARIANT XLMR PRO-92.  
RX MEDLINE=98282090; PubMed=9620768;  
RA D'Adamo P., Menegon A., Lo Nigro C., Grasso M., Gullisano M.,  
RA Tamanini F., Bienvenu T., Gedeon A.K., Oostra B., Wu S.-K., Tandon A.,  
RA Valtorta F., Balch W.E., Chelly J., Toniolo D.;  
RT "Mutations in GD11 are responsible for X-linked non-specific mental  
RT retardation.";  
RL Nat. Genet. 19:134-139(1998).  
RN [9]  
RP VARIANT XLMR PRO-423.  
RX MEDLINE=98334551; PubMed=9668174;  
RA Bienvenu T., Des Portes V., Saint Martin A., McDonnell N., Billuart P.,  
RA Carrie A., Vinet M.-C., Couvert P., Toniolo D., Ropers H.-H.,



Asada M., Kalibuchi K., Takai Y.;  
Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.

[2]  
SEQUENCE FROM N.A.  
MEDLINE-98096592; PubMed-9434952;  
Sedlacek Z., Munstermann E., Mincheva A., Lichter P., Poutska A.;  
"The human rab GDI beta gene with long retroposon-rich introns maps to  
10p15 and its pseudogene to 7p11-p13.";  
Mamm. Genome 9:78-80(1998).

[3]  
SEQUENCE OF 81-439 FROM N.A.  
TISSUE-Pancreas;  
MEDLINE-20453283; PubMed-10996854;  
Caillol N., Pasqualini E., Llobes R., Lombardo D.;  
"Impairment of bile salt-dependent lipase secretion in human  
pancreatic tumoral SOI-6 cells.";  
J. Cell. Biochem. 79:628-647(2000).

[4]  
TISSUE SPECIFICITY.  
MEDLINE-95359978; PubMed-7543319;  
Bachner D., Sedlacek Z., Korn B., Hameister H., Poustka A.;  
"Expression patterns of two human genes coding for different rab GDP-  
dissociation inhibitors (GDIs), extremely conserved proteins involved  
in cellular transport.";  
Hum. Mol. Genet. 4:701-708(1995).

CC -!- FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST RAB  
CC PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE  
CC SUBSEQUENT BINDING OF GTP TO THEM.  
CC -!- TISSUE SPECIFICITY: UBIQUITOUS.  
CC -!- SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATION  
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CC EMBL; D13988; BAA03095.1; -  
CC EMBL; Y13286; CAA73734.1; -  
CC EMBL; Y13287; CAA73735.1; -  
CC EMBL; Y13288; CAA73735.1; JOINED.  
CC EMBL; Y13289; CAA73735.1; JOINED.  
CC EMBL; Y13290; CAA73735.1; JOINED.  
CC EMBL; Y13291; CAA73735.1; JOINED.  
CC EMBL; Y13292; CAA73735.1; JOINED.  
CC EMBL; Y13293; CAA73735.1; JOINED.  
CC EMBL; Y13294; CAA73735.1; JOINED.  
CC EMBL; Y13295; CAA73735.1; JOINED.  
CC EMBL; Y13296; CAA73735.1; JOINED.  
CC EMBL; Y13297; CAA73735.1; JOINED.  
CC EMBL; AFI44713; AAD34588.1; -  
CC HSSP; P21856; LGND.  
CC MIM; 600767; -  
CC InterPro; IPR002005; Rab\_GDI\_REP.  
CC Pfam; PF00996; GDI; 1.  
CC PRINTS; PR00891; RABGDI.  
CC PRINTS; PR00892; RABGDI.  
CC GTPase activation.  
CC CONFLICT 2 N -> D (IN REF. 1).  
CC FT SEQUENCE 445 AA; 50663 MW; CE186A2E3A47FCC9 CRC64;  
CC

RA Asada M., Kalibuchi K., Takai Y.;  
RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.

RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-98096592; PubMed-9434952;  
RA Sedlacek Z., Munstermann E., Mincheva A., Lichter P., Poutska A.;  
RT "The human rab GDI beta gene with long retroposon-rich introns maps to  
RT 10p15 and its pseudogene to 7p11-p13.";  
RL Mamm. Genome 9:78-80(1998).

RN [3]  
RP SEQUENCE OF 81-439 FROM N.A.  
RX TISSUE-Pancreas;  
RA MEDLINE-20453283; PubMed-10996854;  
RT Caillol N., Pasqualini E., Llobes R., Lombardo D.;  
RA "Impairment of bile salt-dependent lipase secretion in human  
RT pancreatic tumoral SOI-6 cells.";  
RL J. Cell. Biochem. 79:628-647(2000).

RN [4]  
RP TISSUE SPECIFICITY.  
RX MEDLINE-95359978; PubMed-7543319;  
RA Bachner D., Sedlacek Z., Korn B., Hameister H., Poustka A.;  
RT "Expression patterns of two human genes coding for different rab GDP-  
RT dissociation inhibitors (GDIs), extremely conserved proteins involved  
RT in cellular transport.";  
RL Hum. Mol. Genet. 4:701-708(1995).

CC -!- FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST RAB  
CC PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE  
CC SUBSEQUENT BINDING OF GTP TO THEM.  
CC -!- TISSUE SPECIFICITY: UBIQUITOUS.  
CC -!- SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATION  
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CC EMBL; AF027361; AAD04247.1; -  
CC HSSP; P21856; LGND.  
CC InterPro; IPR002005; Rab\_GDI\_REP.  
CC Pfam; PF00996; GDI; 1.  
CC PRINTS; PR00891; RABGDI.  
CC GTPase activation.  
CC CONFLICT 2 N -> D (IN REF. 1).  
CC FT SEQUENCE 445 AA; 50321 MW; 9CE6B5407A3B0400 CRC64;  
CC

Query Match 87.8%; Score 36; DB 1; Length 445;  
Best Local Similarity 75.0%; Pred. No. 3.7; Indels 0; Gaps 0;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTPLEELY 8  
Db 46 ITPLEELY 53

RESULT 5  
GDI\_B\_HUMAN STANDARD; PRT; 445 AA.  
ID GDIB\_CANFA  
AC O97556;  
DT 20-AUG-2001 (Rel. 40, Created)  
DT 20-AUG-2001 (Rel. 40, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE RAB GDP DISSOCIATION INHIBITOR BETA (RAB GDI BETA) (GDI-2).  
GN GDI2.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-98019719; PubMed-9802909;  
RA Chen W., Feng Y., Chen D., Wandinger-Ness A.;  
RT "Rab11 is required for trans-golgi network-to-plasma membrane  
RT transport and a preferential target for GDP dissociation inhibitor.";  
RL Mol. Biol. Cell 9:3241-3257(1998).

CC -!- FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST RAB  
CC PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE  
CC SUBSEQUENT BINDING OF GTP TO THEM (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATION  
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CC EMBL; AF027361; AAD04247.1; -  
CC HSSP; P21856; LGND.  
CC InterPro; IPR002005; Rab\_GDI\_REP.  
CC Pfam; PF00996; GDI; 1.  
CC PRINTS; PR00891; RABGDI.  
CC GTPase activation.  
CC CONFLICT 2 N -> D (IN REF. 1).  
CC FT SEQUENCE 445 AA; 50321 MW; 9CE6B5407A3B0400 CRC64;  
CC

Query Match 87.8%; Score 36; DB 1; Length 445;  
Best Local Similarity 75.0%; Pred. No. 3.7; Indels 0; Gaps 0;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTPLEELY 8  
Db 46 ITPLEELY 53

RESULT 6  
GDI\_B\_HUMAN STANDARD; PRT; 445 AA.  
ID GDIB\_HUMAN  
AC P50395; Q43928; Q90M6;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 20-AUG-2001 (Rel. 40, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE RAB GDP DISSOCIATION INHIBITOR BETA (RAB GDI BETA) (GDI-2).  
GN GDI2 OR RABGDI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE-Brain;



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RESULT 7
GDIB_MOUSE
ID GDIB_MOUSE STANDARD; PRT; 445 AA.
AC P50397;
DT 01-OCT-1996 (Rel. 34, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE RAB GDP DISSOCIATION INHIBITOR BETA (RAB GDI BETA) (GDI-2).
CN GDI2 OR RABGDI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Skeletal muscle;
RX MEDLINE=94217740; PubMed=7513052;
RA Shisheva A., Suedhof T.C., Czech M.P.;
RT "Cloning, characterization, and expression of a novel GDP
RT dissociation inhibitor isoform from skeletal muscle.";
RL Mol. Cell. Biol. 14:3459-3468(1994).
CC -1- FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST RAB
CC PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE
CC SUBSEQUENT BINDING OF GTP TO THEM.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC AND MEMBRANE-ASSOCIATED.
CC -1- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
CC -1- SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATION
CC INHIBITOR.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U07951; AAB16908.1; -.
DR HSSP; P21856; LGND.
DR MGD; MGI:99845; Gdi2.
DR InterPro; IPR002005; Rab_GDI_REP.
DR Pfam; PF00996; GDI; 1.
DR PRINTS; PR00891; RABGDIREP.
DR PRINTS; PR00892; RABGDI.
KW GTPase activation.
SQ SEQUENCE 445 AA; 50512 MW; 7FFD92EAE950EE49 CRC64;

Query Match 87.8%; Score 36; DB 1; Length 445;
Best Local Similarity 75.0%; Pred. No. 3.7;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTPLEELY 8
Db 46 ITPLEDLY 53

RESULT 8
GDIC_MOUSE
ID GDIC_MOUSE STANDARD; PRT; 445 AA.
AC Q61598; Q9D8M9;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE RAB GDP DISSOCIATION INHIBITOR BETA-2 (RAB GDI BETA-2) (GDI-3).
CN GDI3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.

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RX MEDLINE=95301579; PubMed=7782346;
RA Janoueix-Lerosey I., Jollivet F., Camonis J., Marche P.N., Goud B.;
RT "Two-hybrid system screen with the small GTP-binding protein Rab6.
RT Identification of a novel mouse GDP dissociation inhibitor isoform and
RT two other potential partners of Rab6.";
RL J. Biol. Chem. 270:14801-14808(1995).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Iwata A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST RAB
CC PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE
CC SUBSEQUENT BINDING OF GTP TO THEM.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC AND MEMBRANE-ASSOCIATED (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATION
CC INHIBITOR.
CC -----
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CC -----
DR EMBL; L36314; AAA78786.1; -.
DR EMBL; AK007871; BAB25321.1; -.
DR HSSP; P21856; LGND.
DR MGD; MGI:105939; Gdi3.
DR InterPro; IPR002005; Rab_GDI_REP.
DR Pfam; PF00996; GDI; 1.
DR PRINTS; PR00891; RABGDIREP.
KW GTPase activation.
FT CONFLICT 298 I -> N (IN REF. 2).
SQ SEQUENCE 445 AA; 50537 MW; 483B7C7456B30525 CRC64;

Query Match 87.8%; Score 36; DB 1; Length 445;
Best Local Similarity 75.0%; Pred. No. 3.7;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTPLEELY 8
Db 46 ITPLEDLY 53

RESULT 9
GDIC_RAT
ID GDIC_RAT STANDARD; PRT; 445 AA.
AC P50399;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)

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Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.

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DL 15-JUL-1998 (Rel. 36, Last annotation update)
DE RAB GDP DISSOCIATION INHIBITOR BETA-2 (RAB GDI BETA-2) (GDI-3).
GN GDI3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RA Nishimura N., Nakamura H., Hirano H., Kato M., Sasaki T., Takai Y.;
RA MEDLINE=94245743; PubMed=8188702;
RT "Molecular cloning and characterization of two rat GDI species from
RT rat brain: brain-specific and ubiquitous types.";
RL J. Biol. Chem. 269:14191-14198(1994).
RN [2]
RP SEQUENCE OF 30-54 AND 58-74, AND CHARACTERIZATION.
RA Ataki K., Nakanishi H., Hirano H., Kato M., Sasaki T., Takai Y.;
RA MEDLINE=95298038; PubMed=7779099;
RT "Purification and characterization of Rab GDI beta from rat brain.";
RL Biochem. Biophys. Res. Commun. 211:296-305(1995).
CC -1- FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST RAB
CC PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE
CC SUBSEQUENT BINDING OF GTP TO THEM.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC AND MEMBRANE-ASSOCIATED.
CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.
CC -1- SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATION
CC INHIBITOR.
CC
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CC
CC EMBL: X74401; CAA52412.1; -
CC HSP: P21856; IGND.
CC InterPro: IP002005; Rab_GDI_REP.
CC Pfam: PF00996; GDI; 1.
CC PRINTS: P00891; RABGDIREP.
CC PRINTS: P00892; RABGDI.
CC GTPase activation.
CC SEQUENCE 445 AA; 50685 MW; D081ABB31DB9CD29 CRC64;
SQ
Query Match 87.8%; Score 36; DB 1; Length 445;
Best Local Similarity 75.0%; Pred. No. 3.7; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 0;
QY 1 LTPLEELY 8
DB 46 ITPLEEDLY 53
RESULT 10
ID DEOB_BACSU STANDARD; PRT; 396 AA.
AC P46353;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PHOSPHOTOMUTASE (EC 5.4.2.7) (PHOSPHOEXORIBOMUTASE).
GN DRM.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BR151;
RA Schuch R., Piggot P.J., Garibian A., Nygaard P.;

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RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / JH642;
RA Kobayashi Y., Mizuno M., Masuda S., Takemaru K., Hosono S.;
RA Sato T., Takeuchi M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: D-RIBOSE 1-PHOSPHATE = D-RIBOSE 5-PHOSPHATE.
CC -1- CATALYTIC ACTIVITY: 2-DEOXY-D-RIBOSE 1-PHOSPHATE = 2-DEOXY-
CC D-RIBOSE 5-PHOSPHATE.
CC -1- PATHWAY: INVOLVED IN PURINE NUCLEOSIDE SALVAGE.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOTOMUTASE FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U32685; AAA74433.1; -
CC EMBL: D84432; BAA12650.1; -
CC EMBL: Z99116; CAB14282.1; -
CC Subtilisin; BG11331; drn.
CC InterPro: IP002599; Metalloenzyme.
CC Pfam: PF01676; Metalloenzyme; 1.
CC Isomerase; Complete proteome.
CC CONFLICT 78 78 M -> L (IN REF. 2).
CC CONFLICT 209 210 MISSING (IN REF. 2).
CC CONFLICT 318 318 E -> G (IN REF. 2).
CC SEQUENCE 396 AA; 44294 MW; C41A3BE4317456E CRC64;
SQ
Query Match 80.5%; Score 33; DB 1; Length 396;
Best Local Similarity 75.0%; Pred. No. 14; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 1;
QY 1 LTPLEELY 8
DB 169 VVPLEELY 176
RESULT 11
ID YA58_METJA STANDARD; PRT; 609 AA.
AC Q58458;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL PROTEIN MJ1058.
GN MJ1058.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RA MEDLINE=96337999; PubMed=8688087;
RA Sutton C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Bult C.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadov P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Smith M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Hurt H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RA jannaschii.";
RL Science 273:1058-1073(1996).
CC -1- SIMILARITY: BELONGS TO THE NODU / CMCH FAMILY.
CC

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CC -----  
CC EMBL: U67549; AAB99062.1; -  
CC TIGR: MJ1058; -  
CC InterPro: IPR003696; Carbamoyltransferase.  
CC Pfam: PF02543; CmcH\_NodU; 1.  
CC Hypothetical protein; Transferase; Complete proteome.  
CC SEQUENCE 609 AA; 71733 MW; C91899CF01CB84EA CRC64;

Query Match 80.58; Score 33; DB 1; Length 609;  
Best Local Similarity 85.78; Pred. No. 23;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 TPLEELY 8  
DB 359 TPFEELY 365  

RESULT 12  
IF2A\_YEAST STANDARD; PRT; 304 AA.  
AC P20459;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE EUKARYOTIC TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-  
DE ALPHA).  
GN SU12 OR TIF211 OR YJR007W OR J1429.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89202411; PubMed=2649894;  
RA Cigan A.M., Pabich E.K., Feng L., Donahue T.F.;  
RT "Yeast translation initiation suppressor su12 encodes the alpha  
RT subunit of eukaryotic initiation factor 2 and shares sequence  
RT identity with the human alpha subunit".  
RL Proc. Natl. Acad. Sci. U.S.A. 86:2784-2788(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S288C / FY1679;  
RA de Haan M., Smits P.H.M., Grivell L.A.;  
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS  
CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA. THIS  
CC COMPLEX BINDS TO A 40S RIBOSOMAL SUBUNIT, FOLLOWED BY MRNA BINDING  
CC TO FORM A 43S PREINITIATION COMPLEX. JUNCTION OF THE 60S RIBOSOMAL  
CC SUBUNIT TO FORM THE 80S INITIATION COMPLEX IS PRECEDED BY  
CC HYDROLYSIS OF THE GTP BOUND TO EIF-2 AND RELEASE OF AN EIF-2-GDP  
CC BINARY COMPLEX. IN ORDER FOR EIF-2 TO RECYCLE AND CATALYZE ANOTHER  
CC ROUND OF INITIATION, THE GDP BOUND TO EIF-2 MUST EXCHANGE WITH GTP  
CC BY WAY OF A REACTION CATALYZED BY EIF-2B.  
CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA  
CC CHAIN.  
CC -1- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.  
CC -1- SIMILARITY: CONTAINS 1 'SI MOTIF' DOMAIN.  
CC -----  
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CC -----

CC EMBL: M25552; AAA70332.1; -  
CC EMBL: X87611; CAA60929.1; -  
CC EMBL: Z49507; CAA89529.1; -  
CC PIR: A32108; A32108.  
CC SGD: S0003767; SU12.  
CC InterPro: IPR003029; S1.  
CC Pfam: PF00575; S1; 1.  
CC SMART: SM00316; S1; 1.  
CC Initiation factor; Protein biosynthesis; RNA-binding;  
CC KW Phosphorylation.  
CC FT MOD\_RES 52 PHOSPHORYLATION (BY GCN2).  
CC SEQUENCE 304 AA; 34717 MW; AF4FIC80303A4E98 CRC64;  
Query Match 78.08; Score 32; DB 1; Length 304;  
Best Local Similarity 100.08; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 PLEELY 8  
DB 122 PLEELY 127  

RESULT 13  
SD22\_YEAST STANDARD; PRT; 338 AA.  
AC P36047;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE PROTEIN PHOSPHATASES PP1 REGULATORY SUBUNIT SDS22.  
GN SDS22 OR EGP1 OR YKL193C.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=YN 295;  
RA Mackelvie S.H., Andrews P.D., Stark M.J.R.;  
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Maia E Silva A., Bossier P., Vilela C., Fernandes L., Soares H.,  
RA Guerreiro P., Rodrigues-Pousada C.;  
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 1-136 FROM N.A.  
RC STRAIN=GRF88;  
RX MEDLINE=93348778; PubMed=8394042;  
RA Cheret G., Mattheakis L.C., Sor F.;  
RT "DNA sequence analysis of the YCN2 region of chromosome XI in  
RT Saccharomyces cerevisiae".  
CC -1- FUNCTION: POTENTIAL REGULATOR OF THE MITOTIC FUNCTION OF YEAST  
CC TYPE 1 PROTEIN PHOSPHATASE.  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -1- SIMILARITY: CONTAINS 8 LEUCINE-RICH REPEATS (LRR).  
CC -1- SIMILARITY: STRONG, TO S.POMBE SDS22 AND C.ELEGANS T09A5.9.  
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CC -----  
CC EMBL: X83609; CAA58588.1; -  
CC EMBL: Z28193; CAA82037.1; -  
CC EMBL: X69765; -; NOT\_ANNOTATED\_CDS.  
CC PIR: S38030; S38030.

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DR SGD; S0001676; SDS22.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003592; LRR_out.
DR Pfam: PF00560; LRR; 9.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00370; LRR; 11.
KW Leucine-rich repeat; Repeat; LRR 1.
FT REPEAT 65 89
FT REPEAT 91 112
FT REPEAT 112 136
FT REPEAT 156 179
FT REPEAT 181 202
FT REPEAT 202 226
FT REPEAT 246 270
FT REPEAT 295 318
SQ SEQUENCE 338 AA; 38887 MW; 1EF434C7276ABAE CRC64;

Query Match 78.0%; Score 32; DB 1; Length 338;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTPLEELY 8
DB 224 LTNLEELY 231

RESULT 14
YCCT_ECOLI
ID YCCT_ECOLI STANDARD; PRT; 366 AA.
AC P76015;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 39.5 KDA PROTEIN IN TREA-PTH INTERGENIC REGION.
GN YCCT OR B1200.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia
OX NCBI_TaxID=562;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RA "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
CC -1- SIMILARITY: BELONGS TO THE DIHYDROXYACETONE KINASE FAMILY.
CC CORRESPONDS TO THE N-TERMINAL PART OF DHAK. YCGS IS THE C-TERMINAL
CC PART.
-----
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CC
CC EMBL; AE000218; AAC74284.1; -.
CC EMBL; D90754; BAA36057.1; -.
CC EcoGene; EGI3901; Ycgt.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 366 AA; 39494 MW; 08EA76FC216E55FC CRC64;

Query Match 78.0%; Score 32; DB 1; Length 366;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TPLEELY 8
DB 298 TPLSELY 304

RESULT 15
RNAL_SCHPO
ID RNAL_SCHPO STANDARD; PRT; 386 AA.
AC P41391;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE RAN GTPASE ACTIVATING PROTEIN 1 (PROTEIN RNAL).
GN RNAL OR SPAC22E12.07.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
[1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP STRAIN=972;
RX MEDLINE=93385646; PubMed=83741168;
RA Melchior F., Weber K., Gerke V.;
RT "A functional homologue of the RNAL gene product in
RT Schizosaccharomyces pombe: purification, biochemical
RT characterization, and identification of a leucine-rich repeat
RT motif.";
RL Mol. Biol. Cell 4:569-581(1993).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=972;
RX Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RA Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
[3]
RN CHARACTERIZATION, AND PARTIAL SEQUENCE.
RP STRAIN=972;
RX MEDLINE=95183543; PubMed=7878053;
RA Bischoff F.R., Krebber H., Kempf T., Hermes L., Ponstingl H.;
RT "Human Rangpase-activating protein RangAP1 is a homologue of yeast
RT Rnaip involved in mRNA processing and transport.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:1749-1753(1995).
[4]
RN X-RAY CRYSTALLOGRAPHY (2.66 ANGSTROMS).
RX MEDLINE=99322670; PubMed=10394366;
RA Hillig R.C., Renault L., Vetter I.R., Drell T. IV, Wittinghofer A.,
RA Becker J.;
RA "The crystal structure of rnaip: a new fold for a GTPase-activating
RT protein.";
RL Mol. Cell 3:781-791(1999).
CC -1- FUNCTION: GTPASE ACTIVATOR FOR THE NUCLEAR RAS-RELATED REGULATORY
CC PROTEIN SP1 (RAN), CONVERTING IT TO THE PUTATIVELY INACTIVE GDP-
CC BOUND STATE.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC; POSSIBLY ENRICHED IN THE
CC NUCLEAR PERIPHERY.
CC -1- SIMILARITY: CONTAINS 8 LEUCINE-RICH REPEATS (LRR).
CC -1- SIMILARITY: TO MAMMALIAN RANGAP1.
-----
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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DR EMBL; X69882; CAA49509.1; -;  
DR EMBL; 270043; CAA93894.1; -;  
DR PIR; S37691; S37691.  
DR PDB; 1YRG; 29-MAR-00.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR003592; LRR\_out.  
DR Pfam; PF00560; LRR; 2.  
DR SMART; SM00370; LRR; 5.  
KW GTPase activation; Repeat; Leucine-rich repeat; 3D-structure.  
FT REPEAT 23 48 LRR 1.  
FT REPEAT 85 112 LRR 2.  
FT REPEAT 113 141 LRR 3.  
FT REPEAT 179 206 LRR 4.  
FT REPEAT 207 235 LRR 5.  
FT REPEAT 236 264 LRR 6.  
FT REPEAT 265 293 LRR 7.  
FT REPEAT 294 322 LRR 8.  
FT DOMAIN 323 374 ASP/GLU-RICH (ACIDIC).  
FT SITE 74 74 CRITICAL RESIDUE FOR GTP HYDROLYSIS.  
SQ SEQUENCE 386 AA; 43235 MW; 8E1C9C506988A7F1 CRC64;

Query Match 78.0%; Score 32; DB 1; Length 386;  
Best Local Similarity 85.7%; Pred. No. 23;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 TPLEELY 8  
    |||||  
Db 122 TPLEHLY 128

Search completed: January 29, 2002, 11:13:49  
Job time: 825 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 11:12:15 ; Search time 285.36 Seconds  
(without alignments)  
4.101 Million cell updates/sec

Title: US-09-763-397A-21  
Perfect score: 41  
Sequence: 1 LTPLEELY 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 segs, 146272329 residues  
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_17.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mhc.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	171	5 Q26002	Q26002 plasmodium
2	41	100.0	171	5 Q26003	Q26003 plasmodium
3	41	100.0	292	5 Q25762	Q25762 plasmodium
4	41	100.0	782	5 Q25730	Q25730 plasmodium
5	41	100.0	782	5 Q26104	Q26104 plasmodium
6	41	100.0	782	5 Q25875	Q25875 plasmodium
7	41	100.0	782	5 Q26007	Q26007 plasmodium
8	41	100.0	782	5 Q9U431	Q9U431 plasmodium
9	41	100.0	782	5 Q9U430	Q9U430 plasmodium
10	41	100.0	782	5 Q9U429	Q9U429 plasmodium
11	41	100.0	782	5 Q9U414	Q9U414 plasmodium
12	39	95.1	446	5 Q9Y0A4	Q9Y0A4 branchiosto
13	38	92.7	444	5 Q21449	Q21449 caenorhabdi
14	37	90.2	448	5 Q02441	Q02441 geodia cydo
15	36	87.8	149	12 Q9EMU2	Q9emu2 ansacta moo
16	36	87.8	230	11 Q9CZ18	Q9cz18 mus musculu
17	36	87.8	448	13 Q93382	Q93382 gallus gall
18	35	85.4	359	5 Q9UAF7	Q9uaf7 branchiosto
19	35	85.4	360	5 Q77158	Q77158 branchiosto

20	35	85.4	443	5 Q9VLB7	Q9vlb7 drosophila
21	35	85.4	448	5 Q24349	Q24349 drosophila
22	34	82.9	276	13 Q9PTH3	Q9pth3 brachydanio
23	34	82.9	335	2 Q9HY96	Q9hy96 pseudomonas
24	34	82.9	390	2 Q9WY14	Q9wy14 thermotoga
25	34	82.9	412	2 Q9PKD8	Q9pkd8 chlamydia m
26	34	82.9	414	2 Q84258	Q84258 chlamydia t
27	34	82.9	990	10 Q40699	Q40699 oryza sativ
28	33	80.5	117	2 Q07542	Q07542 bacillus su
29	33	80.5	139	5 Q9X29	Q9x29 caenorhabdi
30	33	80.5	296	2 Q53053	Q53053 listeria iv
31	33	80.5	338	1 P95904	P95904 sulfolobus
32	33	80.5	392	2 Q99X76	Q99x76 staphylococ
33	33	80.5	393	2 Q9KCN9	Q9kc9 bacillus ha
34	33	80.5	506	5 Q9V6P1	Q9v6p1 drosophila
35	33	80.5	632	3 Q07845	Q07845 saccharomyc
36	32	78.0	139	10 Q48852	Q48852 arabidopsals
37	32	78.0	139	10 Q9SKY2	Q9sky2 arabidopsals
38	32	78.0	204	2 Q68685	Q68685 bacillus ce
39	32	78.0	354	5 Q9TXQ3	Q9txq3 caenorhabdi
40	32	78.0	380	3 Q93982	Q93982 zygoscacchar
41	32	78.0	387	3 Q9UV50	Q9uv50 debaryomyce
42	32	78.0	393	2 Q24821	Q24821 bacillus st
43	32	78.0	407	3 Q59854	Q59854 zygoscacchar
44	32	78.0	411	2 Q928E9	Q928e9 chlamydia p
45	32	78.0	411	2 Q9JSF2	Q9jsf2 chlamydia p

ALIGNMENTS

RESULT 1  
Q26002 PRELIMINARY; PRT; 171 AA.  
ID Q26002  
AC Q26002;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE RHOPTRY PROTEIN (FRAGMENT).  
GN RAP-1.  
OS Plasmodium falciparum.  
OC Eukaryote; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SIERRA LEONE;  
RX MEDLINE=92244303; PubMed=1574089;  
RA Howard R.F.;  
RT "The sequence of the p82 rhoptry protein is highly conserved between two Plasmodium falciparum isolates."  
RL Mol. Biochem. Parasitol. 51:327-330(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SIERRA LEONE;  
RX MEDLINE=93293317; PubMed=7685740;  
RA Howard R.F., Jensen J.B., Franklin H.L.;  
RT "Reactivity profile of human anti-82-kilodalton rhoptry protein antibodies generated during natural infection with Plasmodium falciparum."  
RL Infect. Immun. 61:2960-2965(1993).  
DR EMBL: L10322; AAB59202.1; -.  
FT NON\_TER 1  
FT NON\_TER 171  
SQ SEQUENCE 171 AA; 18510 MW; 8BF5709D8D30B844 CRC64;

Query Match 100.0%; Score 41; DB 5; Length 171;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LTPLEELY 8  
Db 79 LTPLEELY 86

Mon Feb 4 15:23:44 2002

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RL Mol. Biochem. Parasitol. 77:95-98(1996).
DR EMBL; U41074; AAC47090.1; -.
FT NON_TER 1
SQ SEQUENCE 292 AA; 32345 MW; A35C979C3FEC3019 CRC64;

Query Match 100.0%; Score 41; DB 5; Length 292;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTPLEELY 8
Db 196 LTPLEELY 203

RESULT 4
Q25730 PRELIMINARY; PRT; 782 AA.
AC Q25730;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (T-EMBLrel. 16, Last annotation update)
DE RHOPTRY ASSOCIATED PROTEIN-1.
GN RAP-1.
OS Plasmodium falciparum (isolate FC27 / Papua New Guinea).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5837;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FC27;
RA Shi Y., Lal A.A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U20985; AAA63681.1; -.
SQ SEQUENCE 782 AA; 90023 MW; F69E26A2A564C8EA CRC64;

Query Match 100.0%; Score 41; DB 5; Length 782;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTPLEELY 8
Db 202 LTPLEELY 209

RESULT 5
Q26104 PRELIMINARY; PRT; 782 AA.
AC Q26104;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (T-EMBLrel. 14, Last annotation update)
DE RHOPTRY ASSOCIATED PROTEIN 1.
GN RAP-1.
OS Plasmodium reichenowi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5854;
RN [1]
RP SEQUENCE FROM N.A.
RA Shi Y., Lal A.A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U20986; AAA63682.1; -.
SQ SEQUENCE 782 AA; 90160 MW; DE6D1BE2FAC308A9 CRC64;

Query Match 100.0%; Score 41; DB 5; Length 782;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTPLEELY 8
Db 202 LTPLEELY 209

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RESULT 2
Q26003 PRELIMINARY; PRT; 171 AA.
AC Q26003;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (T-EMBLrel. 08, Last annotation update)
DE RHOPTRY PROTEIN (FRAGMENT).
GN RAP-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TANZANIA I/CDC;
RX MEDLINE=92244303; PubMed=1574089;
RA Howard R.F.;
RT "The sequence of the p82 rhostry protein is highly conserved between two Plasmodium falciparum isolates."
RL Mol. Biochem. Parasitol. 51:327-330(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TANZANIA I/CDC;
RX MEDLINE=93293317; PubMed=7685740;
RA Howard R.F., Jensen J.B., Franklin H.L.;
RT "Reactivity profile of human anti-82-kilodalton rhostry protein antibodies generated during natural infection with Plasmodium falciparum."
RL Infect. Immun. 61:2960-2965(1993).
DR EMBL; L10323; AAA29742.1; -.
FT NON_TER 1
FT NON_TER 171
SQ SEQUENCE 171 AA; 18531 MW; 192CBAC68970CB8 CRC64;

Query Match 100.0%; Score 41; DB 5; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTPLEELY 8
Db 79 LTPLEELY 86

RESULT 3
Q25762 PRELIMINARY; PRT; 292 AA.
AC Q25762;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (T-EMBLrel. 14, Last annotation update)
DE STRAIN INDD RHOPTRY-ASSOCIATED PROTEIN 1 (RAP-1) (FRAGMENT).
GN RAP-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=INDD (INDIAN ISOLATE D);
RX MEDLINE=92244303; PubMed=1574089;
RA Howard R.F.;
RT "The sequence of the p82 rhostry protein is highly conserved between two Plasmodium falciparum isolates."
RL Mol. Biochem. Parasitol. 51:327-330(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=INDD (INDIAN ISOLATE D);
RX MEDLINE=96379224; PubMed=8784775;
RA Howard R.F., Peterson C.;
RT "Limited RAP-1 sequence diversity in field isolates of Plasmodium falciparum."

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RESULT 6
Q25875 ID Q25875 PRELIMINARY; PRT; 782 AA.
AC Q25875;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE PR86 RHOPTRY PRECURSOR PROTEIN.
GN P82.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HONDURAS I CDC;
RX MEDLINE=90348711; PubMed=2200961;
RA Ridley R.G., Takacs B., Lahm H.W., Delves C.J., Goman M., Certa V.,
Maile H., Woollett G.R., Scaife J.G.;
RT "Characterisation and sequence of a protective rhoptry antigen from
Plasmodium falciparum.";
RL Mol. Biochem. Parasitol. 41:125-134(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HONDURAS I CDC;
RX MEDLINE=92244303; PubMed=1574089;
RA Howard R.F.;
RT "The sequence of the p82 rhoptry protein is highly conserved between
two Plasmodium falciparum isolates.";
RL Mol. Biochem. Parasitol. 51:327-330(1992).
DR EMBL; M80807; AAA29717.1; -.
SQ SEQUENCE 782 AA; 90096 MW; DIAD099862528D42 CRC64;

Query Match 100.0%; Score 41; DB 5; Length 782;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTPLEELY 8
Db 202 LTPLEELY 209

RESULT 7
Q26007 ID Q26007 PRELIMINARY; PRT; 782 AA.
AC Q26007;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE RHOPTRY ASSOCIATED PROTEIN 1 (ROP1) PRECURSOR (FRAGMENT).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=90348711; PubMed=2200961;
RA Ridley R.G., Takacs B., Lahm H.W., Delves C.J., Goman M., Certa V.,
Maile H., Woollett G.R., Scaife J.G.;
RT "Characterisation and sequence of a protective rhoptry antigen from
Plasmodium falciparum.";
RL Mol. Biochem. Parasitol. 41:125-134(1990).
DR EMBL; M32853; AAA29753.1; -.
KW Signal.
FT SIGNAL. 1 22 POTENTIAL.
FT CHAIN 23 >782 POTENTIAL.
FT NON_TER 782 782
SQ SEQUENCE 782 AA; 90080 MW; 2F2E240D40A4C902 CRC64;

Query Match 100.0%; Score 41; DB 5; Length 782;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTPLEELY 8
Db 202 LTPLEELY 209

RESULT 8
Q25875 ID Q25875 PRELIMINARY; PRT; 782 AA.
AC Q25875;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE RHOPTRY-ASSOCIATED PROTEIN 1 (FRAGMENT).
GN RAPI.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA Saul A.;
RT "Efficacy of vaccines containing Rhoptry-Associated Proteins RAPI and
RAP2 of Plasmodium falciparum in Saimiri boliviensis monkeys.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF205282; AAF23403.1; -.
FT NON_TER 782 782
SQ SEQUENCE 782 AA; 90066 MW; B344948D5806F7DC CRC64;

Query Match 100.0%; Score 41; DB 5; Length 782;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTPLEELY 8
Db 202 LTPLEELY 209

RESULT 9
Q26007 ID Q26007 PRELIMINARY; PRT; 782 AA.
AC Q26007;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE RHOPTRY-ASSOCIATED PROTEIN 1 (FRAGMENT).
GN RAPI.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FUP;
RA Saul A.;
RT "Efficacy of vaccines containing Rhoptry-Associated Proteins RAPI and
RAP2 of Plasmodium falciparum in Saimiri boliviensis monkeys.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF205283; AAF23404.1; -.
FT NON_TER 782 782
SQ SEQUENCE 782 AA; 90131 MW; A0FCB64529C34E59 CRC64;

Query Match 100.0%; Score 41; DB 5; Length 782;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTPLEELY 8
Db 202 LTPLEELY 209

RESULT 10

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Q9U429
ID Q9U429 PRELIMINARY; PRT; 782 AA.
AC Q9U429;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE RHOPTRY-ASSOCIATED PROTEIN 1.
GN RAP1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVO;
RA Saul A.;
RT "Efficacy of vaccines containing Rhoptry-Associated Proteins RAP1 and
RAP2 of Plasmodium falciparum in Saimiri boliviensis monkeys.";
RL RAP2 of Plasmodium falciparum to the EMBL/GenBank/DBJ databases.
DR EMBL; AF205284; AAF23405.1; -. 27F2EA9BC930434E CRC64;
SQ SEQUENCE 782 AA; 90041 MW; 27F2EA9BC930434E CRC64;

Query Match 100.0%; Score 41; DB 5; Length 782;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTPLEELY 8
Db 202 LTPLEELY 209

RESULT 11
Q9U414
ID Q9U414 PRELIMINARY; PRT; 782 AA.
AC Q9U414;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE RHOPTRY ASSOCIATED PROTEIN-1.
GN RAP-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FCCL/HN;
RA Li X.R., Luo S.H., Yu X.B., Shan Z.X., Ma C.-L.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206631; AAF15365.1; -.
SQ SEQUENCE 782 AA; 90082 MW; 8E1F4CF2883903FD CRC64;

Query Match 100.0%; Score 41; DB 5; Length 782;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTPLEELY 8
Db 202 LTPLEELY 209

RESULT 12
Q9Y0A4
ID Q9Y0A4 PRELIMINARY; PRT; 446 AA.
AC Q9Y0A4;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE RAB GDP-DISSOCIATION INHIBITOR.
GN RAB-GDI.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
```

```
OX NCBI_TaxID=7739;
RN [1]
RP SEQUENCE FROM N.A.
RA Sedlacek Z., Shmied S.M., Muenstermann E., Poustka A.;
RT "The amphioxus RAB gdp-dissociation inhibitor (GDI) gene is neural-
RT specific: implications for the evolution of function of chordate RAB
RT GDI genes.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y18521; CAB46230.1; -.
DR HSSP; P21856; LGND.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR002005; Rab_GDI_REP.
DR Pfam; PF00996; GDI; 1.
DR PRINTS; PR00891; RABGDIREP.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 446 AA; 49759 MW; 69256AFFC0188D3A CRC64;

Query Match 95.1%; Score 39; DB 5; Length 446;
Best Local Similarity 87.5%; Pred. No. 8.9;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTPLEELY 8
Db 46 LTPLEELY 53

RESULT 13
Q21449
ID Q21449 PRELIMINARY; PRT; 444 AA.
AC Q21449;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE RABGDI PROTEIN.
GN GDI-1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Boguski M.S.;
RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA McMurray A.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U00002; AAA17051.1; -.
DR EMBL; Z99281; CAB16511.1; -.
DR HSSP; P21856; LGND.
DR InterPro; IPR002005; Rab_GDI_REP.
DR Pfam; PF00996; GDI; 1.
DR PRINTS; PR00891; RABGDIREP.
SQ SEQUENCE 444 AA; 50025 MW; 0F3CF46B75161DD CRC64;

Query Match 92.7%; Score 38; DB 5; Length 444;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTPLEELY 8
Db 46 LTPLEELY 53

RESULT 14
O02441
ID O02441 PRELIMINARY; PRT; 448 AA.
AC O02441;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
```

DE GDP-DISSOCIATION INHIBITOR.  
 GN GDI.  
 OS Geodia cydonium (Sponge).  
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;  
 OC Astrophorida; Geodiidae; Geodia.  
 OX NCBI\_TaxID=6047;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Krasko A., Scheffer U., Koziol C., Pancer Z., Batel R., Badria F.A.,  
 RA Mueller W.E.G.; 37:157-168(1997).  
 RL Aquatic Toxicol. 37:157-168(1997).  
 DR EMBL; X94983; CAA64439.1; -.  
 DR HSSP; P21856; 1GND.  
 DR InterPro; IPR002005; Rab\_GDI\_REP.  
 DR Pfam; PF00996; GDI; 1  
 DR PRINTS; PR00891; RABGDIREP.  
 DR SEQUENCE 448 AA; 50215 MW; 0F94A980DC68E1A2 CRC64;

Query Match 90.2%; Score 37; DB 5; Length 448;  
 Best Local Similarity 87.5%; Pred. No. 23;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTPLEELY 8  
 :|:|:|:|:|  
 Db 46 LSPLEELY 53

## RESULT 15

Q9EMU2  
 ID Q9EMU2 PRELIMINARY; PRT; 149 AA.  
 AC Q9EMU2;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE AMV107.  
 GN AMV107.  
 OS Anisacta moorei entomopoxvirus (AnEPV).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;  
 OC Entomopoxvirus B.  
 OX NCBI\_TaxID=28321;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-20396580; PubMed-10936094;  
 RA Bawden A.L., Glassberg K.J., Diggins J., Shaw R., Farmerie W.,  
 RA Moyer R.W.;  
 RT "Complete Genomic Sequence of the Anisacta moorei Entomopoxvirus:  
 RT Analysis and Comparison with Other Poxviruses.";  
 RL Virology 274:120-139(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Bawden A.L., Glassberg K.J., Diggins J., Shaw R., Farmerie W.,  
 RA Moyer R.W.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF250284; AAG02813.1; -.  
 SQ SEQUENCE 149 AA; 17470 MW; 877185CEA034F840 CRC64;

Query Match 87.8%; Score 36; DB 12; Length 149;  
 Best Local Similarity 75.0%; Pred. No. 11;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTPLEELY 8  
 :|:|:|:|:|  
 Db 85 ITPVEELY 92

Search completed: January 29, 2002, 11:12:16  
 Job time: 772 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 29, 2002, 10:21:56 ; Search time 66.28 seconds  
(without alignments)  
18.999 Million cell updates/sec

Title: US-09-763-397A-22

Perfect score: 79

Sequence: 1 SSPSTKSPSNVKSAS 17

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A\_Geneseq\_ll01.\*
- 1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.\*
  - 2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.\*
  - 3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.\*
  - 4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.\*
  - 5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT.\*
  - 6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT.\*
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  - 8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT.\*
  - 9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT.\*
  - 10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT.\*
  - 11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT.\*
  - 12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT.\*
  - 13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT.\*
  - 14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT.\*
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  - 19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.\*
  - 20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.\*
  - 21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.\*
  - 22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	94.9	16	21	AAV70298
2	68.5	86.7	350	21	AAV70278
3	68.5	86.7	782	11	AAV70291
4	49	62.0	530	13	AAV28888
5	48	60.8	140	22	AAV98924
6	48	60.8	328	21	AAV54617
7	48	60.8	328	22	AAV98923
8	48	60.8	328	22	AAE01347
9	46	58.2	139	21	AAG23324
10	46	58.2	141	21	AAG23323
11	46	58.2	147	21	AAG23322

12	46	58.2	243	22	AAU01602	Human secreted pro
13	46	58.2	273	21	AAV70705	Maize replication
14	46	58.2	273	21	AAV70706	Maize replication
15	46	58.2	273	21	AAV70707	Maize replication
16	46	58.2	273	21	AAV70709	Maize replication
17	46	58.2	273	21	AAV70710	Maize replication
18	46	58.2	303	22	AAV40257	Human polypeptide
19	46	58.2	310	22	AAV40257	Human polypeptide
20	46	58.2	310	22	AAU12247	Human PRO4322 poly
21	46	58.2	310	22	AAU01092	Gene 21 Human secr
22	46	58.2	310	22	AAV93940	Human protein sequ
23	46	58.2	310	22	AAV75506	Human secreted pro
24	46	58.2	310	22	AAV75556	Human secreted pro
25	46	58.2	311	22	AAU01060	Human secreted pro
26	46	58.2	318	21	AAV70708	Maize replication
27	46	58.2	473	21	AAV42243	Human ORF2007
28	45	57.0	30	17	AAV08984	Lysine/Serine cont
29	45	57.0	75	18	AAV25779	Peptide carrier #2
30	45	57.0	205	22	AAV75365	Human colon cancer
31	45	57.0	583	21	AAV32210	Human BMAL1a trans
32	45	57.0	626	21	AAV32209	Human BMAL1b trans
33	45	57.0	626	21	AAV32211	Human JAP3 transcr
34	45	57.0	2559	20	AAV41012	Amino acid sequenc
35	44	55.7	176	22	AAV41702	Human polypeptide
36	44	55.7	197	21	AAV09442	Arabidopsis thalia
37	44	55.7	244	22	AAV39916	Human polypeptide
38	44	55.7	285	22	AAV92683	Human protein sequ
39	44	55.7	817	22	AAV38657	Human polypeptide
40	44	55.7	819	22	AAV40442	Human polypeptide
41	44	55.7	819	22	AAV40443	Human polypeptide
42	44	55.7	863	22	AAV38656	Human polypeptide
43	44	55.7	2432	21	AAV85565	Human homologue of
44	43	54.4	30	17	AAV08983	Lysine/Serine cont
45	43	54.4	33	22	AAV19918	Peptide #6352 enco

ALIGNMENTS

RESULT 1  
AAV70298  
ID AAV70298 standard; peptide: 16 AA.  
AC AAV70298;  
DT 06-JUN-2000 (first entry)  
XX Plasmodium falciparum RAP-1 antigenic epitope, P604.  
DE Recombinant protein; CDC/NIAID/VAC-1; multivalent; malaria; vaccine;  
KW T-cell epitope; tetanus toxoid; antigenic epitope; treatment;  
KW circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2;  
KW liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1;  
KW apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175;  
KW ERA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen;  
KW Pf27; antiparasitic; prevention; anti-CDC/NIAID/VAC-1 antibody.  
XX Plasmodium falciparum.  
OS WO200011179-A1.  
PN 02-MAR-2000.  
PD 19-AUG-1999; 99WO-US18869.  
PF 21-AUG-1998; 98US-0097703.  
PR (NAIM-) NAT INST IMMUNOLOGY.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
XX Lal AA, Shi YP, Hasnain SE;  
XX WPI; 2000-237654/20.

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XX
PT Novel recombinant protein as vaccine for treating malarial infection
PT comprises antigenic peptides obtained from different stages of
PT Plasmodium falciparum life cycle
XX
XX Claim 2; Page 17; 52pp; English.
XX
XX The present sequence is the antigenic epitope p604, derived from
XX rhoptry associated protein-1 (RAP-1) of the asexual blood stage of
XX Plasmodium falciparum. It is used in the construction of recombinant
XX protein CDC/NiMALVAC-1, which is a multivalent, multistage malarial
XX vaccine. The recombinant protein comprises, melittin signal peptide,
XX (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes
XX from circumsporozoite protein (CSP), sporozoite surface protein-2
XX (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1
XX (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding
XX antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete
XX specific antigen, Pf27. These epitopes were obtained at different stages
XX of the life cycle of P. falciparum. CDC/NiMALVAC-1 vaccine has
XX antiparasitic activity and can be used for treatment and prevention of
XX malarial infections. Anti-CDC/NiMALVAC-1 antibodies can be used for
XX detecting P. falciparum in biological samples.
XX
XX Sequence 16 AA;
XX
Query Match 94.9%; Score 75; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSPSSTKSSPSNVKSA 16
DB 1 SSPSSTKSSPSNVKSA 16
IIIIIIIIIIIIIIIIIIII
IIIIIIIIIIIIIIIIIIII

RESULT 2
AA70278
ID AAY70278 standard; Protein; 350 AA.
AC AAY70278;
XX
XX 06-JUN-2000 (first entry)
XX
XX Recombinant vaccine CDC/NiMALVAC-1.
XX
XX Recombinant protein; CDC/NiMALVAC-1; multivalent; malaria; vaccine;
XX T-cell epitope; tetanus toxoid; antigenic epitope; treatment;
XX circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2;
XX liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2;
XX apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175;
XX EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen;
XX Pf27; antiparasitic; prevention; anti-CDC/NiMALVAC-1 antibody;
XX honey bee.
XX
XX Chimeric - Apis sp.
XX Chimeric - Clostridium tetani.
XX Chimeric - Plasmodium falciparum.
XX
XX Key Location/Qualifiers
XX Peptide 1..22
XX /label= Melittin_signal_peptide
XX /note= "Derived from Honey bee"
XX
XX Protein 23..350
XX /label= Mature_CDC/NiMALVAC-1
XX /note= "Recombinant multivalent malarial vaccine"
XX
XX WO200011179-A1.
XX
XX 02-MAR-2000.
XX
XX 19-AUG-1999; 99WO-US18869.
XX
XX 21-AUG-1998; 98US-0097703.
XX

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XX
PA (NATM-) NAT INST IMMUNOLOGY.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Lal AA, Shi YP, Hasnain SE;
XX
XX WPI: 2000-237654/20.
XX N-PSDB; AA051336.
XX
XX Novel recombinant protein as vaccine for treating malarial infection
XX comprises antigenic peptides obtained from different stages of
XX Plasmodium falciparum life cycle
XX
XX Claim 3; Page 43-44; 52pp; English.
XX
XX The present sequence is that of recombinant protein CDC/NiMALVAC-1,
XX which is a multivalent, multistage malarial vaccine. The recombinant
XX protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope
XX from tetanus toxoid and 21 antigenic epitopes from circumsporozoite
XX protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage
XX antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical
XX membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175),
XX rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pf27.
XX These epitopes were obtained at different stages of the life cycle of
XX Plasmodium falciparum. CDC/NiMALVAC-1 vaccine has antiparasitic
XX activity and can be used for treatment and prevention of malarial
XX infections. Anti-CDC/NiMALVAC-1 antibodies can be used for detecting
XX P. falciparum in biological samples.
XX
XX Sequence 350 AA;
XX
Query Match 86.7%; Score 68.5; DB 21; Length 350;
Best Local Similarity 94.4%; Pred. No. 0.012;
Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 SSPSSTK-SSPSNVKSSAS 17
DB 299 SSPSSTKSSPSNVKSSAS 316
IIIIIIIIIIIIIIIIIIII
IIIIIIIIIIIIIIIIIIII

RESULT 3
AAR06991
ID AAR06991 standard; protein; 782 AA.
XX
XX AAR06991;
XX
XX 16-JAN-1991 (first entry)
XX
XX Polypeptide antigenic to rhoptry organelles of Plasmodium.
XX
XX Malaria; vaccine; rhoptry organelles.
XX
XX Plasmodium falciparum.
XX
XX EP388738-A.
XX
XX 26-SEP-1990.
XX
XX 09-MAR-1990; 90EP-0104561.
XX
XX 22-AUG-1989; 89GB-0019064.
XX 14-MAR-1989; 89GB-0005857.
XX
XX (HOFF ) HOFFMANN-LA ROCHE AG.
XX
XX Ridley RG, Scaife JG;
XX
XX WPI: 1990-291721/39.
XX N-PSDB; AAQ06000.
XX
XX Antigenic polypeptide and DNA encoding it - having a determinant
XX cross reactive with those on the rhoptry organelles of the
XX

```

PT merozoite form of the malaria parasite P falciparum.

PS Claim 1; Fig 2a-b; 29pp; English.

CC Gene product may be isolated from a transformed E.coli (Y1088)  
 CC expression system using plasmid pMC9, and may then be used for  
 CC immunisation against malaria. The product may also be used  
 CC diagnostically to detect Abs directed against the parasite.

XX Sequence 782 AA;

Query Match 86.7%; Score 68.5; DB 11; Length 782;  
 Best Local Similarity 94.4%; Pred. No. 0.03;  
 Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SSPSTK-SSPSNVKSAS 17  
 Db 145 sspsstkspsnvksas 162  
 ||||| |||||

RESULT 4  
 AAR2888  
 ID AAR28888 standard; Protein; 530 AA.

XX AC AAR28888;

XX DT 25-MAR-1993 (first entry)

XX DE Ri paraneoplastic antigenic polypeptide.

XX KW R18; paraneoplastic opsoclonus; PO; cerebellar; expression vector;  
 KW library; Ri; paraneoplastic antigenic polypeptide; phagemid;  
 KW lambda-R18; helper phage; R408; anti-Ri; antiserum; fusion protein;  
 KW antibody; dideoxy method; open reading frame; PCR; probe.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Region 72..107

FT /note= "HOM #1"

FT Region 197..232

FT /note= "HOM #2"

FT Region 447..482

FT /note= "HOM #3"

XX PN W09219635-A.

XX PD 12-NOV-1992.

XX PF 21-APR-1992; 92WO-US03249.

XX PR 25-APR-1991; 91US-0691559.

XX PA (SLOK ) SLOAN KETTERING INST CANCER.

XX PI Darnell RB, Furneaux HW, Posner JB;

XX DR WPI; 1992-398791/48.

XX DR N-PSDB: AAQ30802.

PT Ri para-neoplastic antigenic polypeptide and antibody specific

PT for para-neoplastic antigen - used in the diagnosis and treatment

PT of para-neoplastic opsoclonus

XX Claim 5; Fig 7; 50pp; English.

XX This sequence is the Ri paraneoplastic antigenic polypeptide. The Ri  
 CC gene is associated with paraneoplastic opsoclonus (PO). The DNA  
 CC sequence encoding this polypeptide was isolated via an Ri clone, R18,  
 CC which was isolated from a cerebellar cDNA expression vector library  
 CC derived from antiserum from a single patient with PO. Phagemid was  
 CC excised from lambda-R18 using the helper phage R408, the resulting

CC plasmid being designated pri8 (see also AAQ30801). pri8 was cloned and  
 CC propagated in E. coli. pri8 encoded a protein of mol. wt. 40 kD which  
 CC is recognised by anti-Ri antiserum. This R18 fusion protein was used  
 CC as an antigen to affinity purify antibody from the anti-Ri antiserum.  
 CC The DNA sequence of pri8 was determined by the dideoxy method and an  
 CC open reading frame encoding approx. 340 amino acids was identified.  
 CC Regions of this sequence could be used to make PCR probes such that  
 CC additional clones representing the full length Ri gene could be  
 CC isolated.

XX Sequence 530 AA;

Query Match 62.0%; Score 49; DB 13; Length 530;  
 Best Local Similarity 58.8%; Pred. No. 16;  
 Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SSPSTKSSPSNVKSAS 17  
 Db 176 sspttksspsqpmmts 192  
 ||||| |||||

RESULT 5

AAB98924  
 ID AAB98924 standard; peptide; 140 AA.

XX AC AAB98924;

XX DT 09-OCT-2001 (first entry)

XX DE Arabidopsis thaliana abi4 allele-encoded protein.

XX KW AB14 gene; transactivator; APETALA2 domain; AP2 domain; chromosome 2;  
 KW C-repeat/DRE regulatory element; abscisic acid insensitivity;  
 KW salt tolerance; seed germination; saline soil; abi4 allele.

XX OS Arabidopsis thaliana.

XX FH Key Location/Qualifiers

FT Domain 55..110

FT /label= APETALA2\_domain

FT /note= "Binds to C-repeat/DRE regulatory elements;  
 acts as a transactivator."

XX PN W0200149850-A1.

XX PD 12-JUL-2001.

XX PF 03-JAN-2001; 2001WO-ES00003.

XX PR 03-JAN-2000; 2000ES-0000004.

XX PA (UYEL-) UNIV ELCHE MIGUEL HERNANDEZ.

XX PI Quesada Perez V, Ponce Molet RM, Micol Molina JL;

XX DR WPI; 2001-441881/47.

XX New null allele of the Arabidopsis thaliana AB14 gene, useful for

PT imparting insensitivity to abscisic acid and ability to germinate and

PT grow on saline soils

XX Disclosure; Fig 5; 26pp; Spanish.

XX The invention relates to a null, or extremely hypomorphic, allele of  
 CC the AB14 gene of Arabidopsis thaliana that confers insensitivity to  
 CC abscisic acid and tolerance to salinity during germination. The allele,  
 CC designated san5 or abi4-2, has a deletion of one of the three adenines at  
 CC positions 277-279 relative to the wild-type allele (designated AB14),  
 CC which causes a change in the reading frame leading to a shorter, variant  
 CC C-terminus from amino acid residue 44 onwards. The abi4-2 protein  
 CC (AAB98925) does not contain the APETALA2 (AP2) domain located between  
 CC residues 55-110 in the wild-type AB14 protein (AAB98923) which mediates

transactivational activity at C-repeat/DRE regulatory elements. Seeds of Arabidopsis thaliana homozygous for the ab14-2 (san5) allele are tolerant of high concentrations of sodium chloride (150 mM), mannitol (400 mM), potassium chloride (150 mM) and sodium sulphate (75 mM). The ab14-2 (san5) allele is used to produce Arabidopsis plants that are able to germinate and grow in highly saline soils in which wild-type plants cannot survive. Orthologous alleles from other crop plants can be used to impart similar properties. The present sequence represents the ab14 protein encoded by the mutant allele ab14. This protein contains the APETALA2 domain, but is C-terminally truncated with respect to the wild-type ABI4 protein.

XX Sequence 140 AA;

Query Match 60.8%; Score 48; DB 22; Length 140;  
Best Local Similarity 64.7%; Pred. No. 5.3;  
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 SSPSTKSPSNVKSAS 17  
Db 113 sspssvssssvsas 129  
||||| ||| :||

RESULT 6  
AAV54617 standard; Protein; 328 AA.  
ID AAV54617  
AC AAV54617;  
XX

XX 02-FEB-2000 (first entry)

XX Arabidopsis Abi4 protien sequence.

XX Abi4 gene; seed development regulation; seed nutrient reserve production;  
XX desiccation protectant; vegetative stress tolerance.

XX Arabidopsis thaliana.  
OS  
XX WO9955840-A1.  
XX

XX 04-NOV-1999.

XX 27-APR-1999; 99WO-US08954.

XX 27-APR-1998; 98US-0083334.

XX (REGC ) UNIV CALIFORNIA.  
XX (GEO ) GEN HOSPITAL CORP.

XX WPI: 2000-013434/01.

XX N-PSDB; AAZ37307, AAZ37308.

XX Arabidopsis thaliana ABI4 gene, mutants and variants, useful for  
XX creating transgenic plants with e.g. modified regulation of seed  
XX viability and vegetative stress tolerance

XX Claim 6; Fig 4; 68pp; English.

XX This sequence represents the Arabidopsis thaliana Abi4 protein of the  
XX invention. Abi4 is involved in regulating seed development, production of  
XX seed nutrient reserves and desiccation protectants. The nucleic acid  
XX can be used to create transgenic plants with modified regulation of seed  
XX viability, production of nutrient reserves and desiccation protectants in  
XX seeds and vegetative stress tolerance, e.g. to drought or salinity, and  
XX response to abscisic acid.

XX Sequence 328 AA;

Query Match 60.8%; Score 48; DB 21; Length 328;  
Best Local Similarity 64.7%; Pred. No. 13;  
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 SSPSTKSPSNVKSAS 17  
Db 113 sspssvssssvsas 129  
||||| ||| :||

RESULT 7

AA98923  
ID AAB98923 standard; peptide; 328 AA.

XX AAB98923;

XX 09-OCT-2001 (first entry)

XX Arabidopsis thaliana ABI4 wild-type protein.

XX ABI4 gene; transactivator; APETALA2 domain; AP2 domain; chromosome 2;  
XX C-repeat/DRE regulatory element; abscisic acid insensitivity;  
XX salt tolerance; seed germination; saline soil; wild-type allele.

XX Arabidopsis thaliana.

XX Key Location/Qualifiers  
XX Domain 55..110  
XX /label= APETALA2 domain  
XX /note= "Binds to C-repeat/DRE regulatory elements;  
XX acts as a transactivator"

XX WO200149850-A1.

XX 12-JUL-2001.

XX 03-JAN-2001; 2001WO-ES000003.

XX 03-JAN-2000; 2000ES-0000004.

XX (UYEL-) UNIV ELCHE MIGUEL HERNANDEZ.

XX Quesada Perez V, Ponce Molet RM, Micol Molina JL;

XX WPI: 2001-441881/47.

XX New null allele of the Arabidopsis thaliana ABI4 gene, useful for  
XX imparting insensitivity to abscisic acid and ability to germinate and  
XX grow on saline soils

XX Disclosure; Fig 5; 26pp; Spanish.

XX The invention relates to a null, or extremely hypomorphic, allele of  
XX the ABI4 gene of Arabidopsis thaliana that confers insensitivity to  
XX abscisic acid and tolerance to salinity during germination. The allele,  
XX designated san5 or ab14-2, has a deletion of one of the three adenines at  
XX positions 277-279 relative to the wild-type allele (designated ABI4),  
XX which causes a change in the reading frame leading to a shorter, variant  
XX C-terminus from amino acid residue 44 onwards. The ab14-2 protein  
XX (AAB98923) does not contain the APETALA2 (AP2) domain located between  
XX residues 55-110 in the wild-type ABI4 protein (AAB98923) which mediates  
XX transactivational activity at C-repeat/DRE regulatory elements. Seeds of  
XX Arabidopsis thaliana homozygous for the ab14-2 (san5) allele are tolerant  
XX of high concentrations of sodium chloride (150 mM), mannitol (400 mM),  
XX potassium chloride (150 mM) and sodium sulphate (75 mM). The ab14-2  
XX (san5) allele is used to produce Arabidopsis plants that are able to  
XX germinate and grow in highly saline soils in which wild-type plants  
XX cannot survive. Orthologous alleles from other crop plants can be used  
XX to impart similar properties. The present sequence represents the  
XX wild-type ABI4 protein.

XX Sequence 328 AA;

Query Match 60.8%; Score 48; DB 22; Length 328;  
Best Local Similarity 64.7%; Pred. No. 13;  
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;



Qy 1 SSPSTKSSPSNVKAS 17  
||||| ||| :||  
Db 113 sspssvsssssvsaas 129

RESULT 8  
AAE01347  
ID AAE01347 standard; Protein; 328 AA.  
AC AAE01347;  
XX  
DT 31-JUL-2001 (first entry)  
XX  
DE Arabidopsis thaliana ABA (abscisic acid)-insensitive 4, ABI4 protein.  
KW Abscisic acid; ABA; ABA-insensitive; ABI4; signal transduction;  
KW kernel embryo promoter; cereal plant; maize; rice; cotton; citrus tree;  
KW tomato; pine; soybean; peanut; olive.  
XX  
OS Arabidopsis thaliana.  
XX  
PN WO200136596-A2.  
XX  
PD 25-MAY-2001.  
XX  
PF 17-NOV-2000; 2000WO-US31739.  
XX  
PR 17-NOV-1999; 99US-0166080.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Helentjaris T;  
XX  
DR WPI: 2001-329218/34.  
DR N-PSDB; AAD05663.  
XX  
XX DNA constructs containing an abscisic acid-associated sequence are used  
PT to modulate a response in a plant to abscisic acid so that the plants  
PT are protected against any harmful or detrimental effects of stress and  
PT environmental conditions -  
XX  
PS Claim 3; Page 57-58; 60pp; English.  
XX  
CC The invention relates to a method for modulating a response in a target  
CC plant to abscisic acid (ABA) by introducing a DNA construct comprising  
CC an ABA-associated sequence operably linked to an early kernel/embryo  
CC promoter into the plant. The method also involves modulating ABA  
CC perception and signal transduction in developing seeds. The method is  
CC used to produce plants, particularly cereal plants such as maize, which  
CC have a modified response to ABA so that an increase in yield can be  
CC produced. The plants are protected against any harmful/detrimental  
CC effects of stress and adverse environmental conditions. The ABA function  
CC is disrupted in a tissue and developmental preferred manner so that  
CC female reproductive tissue is insulated from the stress or adverse  
CC environmental conditions. Other plants which can be transformed include  
CC rice, cotton, citrus trees, tomatoes, pines, soybean, peanut and olive.  
CC The present sequence is Arabidopsis thaliana ABA-insensitive 4 (ABI4)  
CC protein.  
XX  
SQ Sequence. 328 AA;

Query Match 60.8%; Score 48; DB 22; Length 328;  
Best Local Similarity 64.7%; Pred. No. 13;  
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SSPSTKSSPSNVKAS 17  
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Db 113 sspssvsssssvsaas 129

RESULT 9

AAG23324  
ID AAG23324 standard; Protein; 139 AA.  
XX  
AC AAG23324;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26590.  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
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PR 18-JUN-1999; 99US-0139460.
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PR 29-OCT-1999; 99US-0162142.

Query Match 58.2%; Score 46; DB 21; Length 139;
Best Local Similarity 56.2%; Pred. No. 10;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 SPSSTKSPSNVKSAS 17
Db 69 spsstpsdptsikcaa 84

RESULT 10
AAG23323
ID AAG23323 standard; Protein: 141 AA.
XX
AC AAG23323;
XX
DT 17-OCT-2000 (first entry)
XX
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 26589.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EPI033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
XX 25-FEB-2000; 2000EP-0301439.  
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Best Local Similarity 56.2%; Pred. No. 11;
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Db 77 spstpsdptsikcaa 92
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AAU01602
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XX
AC AAU01602;
XX
DT 18-JUL-2001 (first entry)
XX
DE Human secreted protein encoded by gene #16.
XX
KW Human secreted protein; autoimmune disorder; hyperproliferative disorder;
KW cardiovascular disorder; cerebrovascular disorder; angiogenesis;
KW nervous system disorder; bacterial infection; viral infection;
KW fungal infection; ocular disorder; wound healing; tissue regeneration;
KW epithelial cell proliferation; skin ageing; chemotaxis; IgG Fc region.
XX
OS Homo sapiens.
XX
PN WO200123547-A1.
XX
PD 05-APR-2001.
XX
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PF 26-SEP-2000; 2000WO-US26337.  
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 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Komatsoulis GA, Ruben SM, Rosen CA;  
 XX  
 DR WPI; 2001-266151/27.  
 XX N-PSDB; AAS02655.  
 XX  
 XX Nucleic acids encoding 26 human secreted polypeptides, useful for  
 PT preventing, diagnosing and/or treating e.g. Gaucher's disease,  
 PT Alzheimer's disease, Schmiter syndrome, Creutzfeldt-Jacob disease,  
 PT diabetes mellitus and multiple sclerosis -  
 XX  
 PS Disclosure; Page 399; 412pp; English.  
 XX  
 CC The sequence represents a human secreted protein encoded by a nucleic  
 CC acid of the invention. Secreted proteins and their related nucleic acids  
 CC can be used in the diagnosis of or susceptibility to a pathological  
 CC condition by determining the presence or absence of a mutation in a  
 CC nucleic acid or the presence or amount of expression of a secreted  
 CC protein. The sequences are used to prevent, treat or ameliorate a medical  
 CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,  
 CC chickens or sheep. The antibodies to the polypeptides can also be used in  
 CC alleviating symptoms associated with disorders and in diagnostic  
 CC immunoassays e.g. radioimmunoassays or enzyme linkedCC immunosorbent  
 CC assays (ELISA). The disorders include autoimmune diseases e.g. rheumatoid  
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or  
 CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular  
 CC disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders  
 CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and  
 CC fungi and ocular disorders e.g. corneal infection. The peptides can also  
 CC be used to aid wound healing and epithelial cell proliferation, to help  
 CC prevent skin ageing due to sunburn, to maintain organs before  
 CC transplantation, to regenerate tissues, in chemotaxis and as a food  
 CC additive or preservative to alter storage capabilities.  
 XX  
 SQ Sequence 243 AA;

Query Match 58.2%; Score 46; DB 22; Length 243;  
 Best Local Similarity 64.7%; Pred. No. 19;  
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 SSPSTKSSPSNVKAS 17  
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 Db 156 sspslstsppevfias 172

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 AC AAY70705;  
 XX  
 XX 18-JUL-2000 (first entry)  
 DT  
 DE Maize replication protein A middle subunit homologue-1 (ZMRPAMSH1).  
 XX  
 XX Maize; Replication protein A; RPA; middle subunit; ZMRPAMSH; virucide;  
 KW fungicide; insecticide; chromosome 5; DNA-binding protein; DNA repair;  
 KW DNA metabolism; DNA replication; cell cycle; homologous recombination;  
 KW pathogen resistance; fungi; virus; nematode; insect; gene therapy;  
 KW genetic manipulation.  
 XX  
 OS Zea mays.  
 XX  
 XX WO200015816-A2.  
 XX  
 XX 23-MAR-2000.  
 PD  
 XX  
 XX 15-SEP-1999; 99WO-US21277.  
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 PR  
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 XX (PION-) PIONEER HI-BRED INT INC.  
 PA  
 PI Mahajan P;

PF 15-SEP-1999; 99WO-US21277.  
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 PR 11-MAR-1999; 99US-0123896.  
 XX  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 PI Mahajan P;  
 XX  
 DR WPI; 2000-271452/23.  
 XX N-PSDB; AAZ52287.  
 DR  
 XX New maize replication protein A useful for genetic transformation, gene  
 PT targeting in plants and modulating DNA metabolism -  
 PT  
 XX Claim 1c; Page 88; 101pp; English.  
 PS  
 XX The present sequence is the maize replication protein A (RPA) middle  
 CC subunit homologue-1 (ZMRPAMSH1). RPA is a single-stranded DNA-binding  
 CC protein required for multiple processes in DNA metabolism, like DNA  
 CC replication, repair mechanism (e.g. nucleotide excision and double  
 CC stranded (ds) DNA break repair) and recombination. The gene for the  
 CC ZMRPAMSH homologue is mapped to chromosome 5. This sequence has  
 CC fungicide, virucide and insecticidal activity. DNA encoding RPA is  
 CC used for modulating DNA metabolism, influencing cell cycle, enhancing  
 CC homologous recombination and increasing pathogen resistance in plants.  
 CC Pests that can be controlled include fungal pathogens, viruses, RPA  
 CC nematodes and insects. Antisense sequences can be used to block RPA  
 CC expression and promote non-specific recombination events. RPA protein  
 CC can be used to improve genetic manipulation and also in gene therapy.  
 XX  
 SQ Sequence 273 AA;

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 Best Local Similarity 58.8%; Pred. No. 22;  
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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 Db 190 stptsikssppvtsgs 206

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 XX  
 AC AAY70706;  
 XX  
 DT 18-JUL-2000 (first entry)  
 DT  
 XX Maize replication protein A middle subunit homologue-2 and 3.  
 XX  
 XX Maize; Replication protein A; RPA; middle subunit; ZMRPAMSH; virucide;  
 KW fungicide; insecticide; chromosome 5; DNA-binding protein; DNA repair;  
 KW DNA metabolism; DNA replication; cell cycle; homologous recombination;  
 KW pathogen resistance; fungi; virus; nematode; insect; gene therapy;  
 KW genetic manipulation.  
 XX  
 OS Zea mays.  
 XX  
 XX WO200015816-A2.  
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 XX 23-MAR-2000.  
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 XX 15-SEP-1999; 99WO-US21277.  
 PF  
 XX 17-SEP-1998; 98US-0100690.  
 PR  
 XX 11-MAR-1999; 99US-0123896.  
 PR  
 XX (PION-) PIONEER HI-BRED INT INC.  
 PA  
 PI Mahajan P;

Search completed: January 29, 2002, 10:59:18  
Job time: 2242 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 10:24:14 ; Search time 32.24 seconds  
(without alignments)  
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Title: US-09-763-397A-22

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	43	54.4	145	3	US-09-300-672-2
4	41	51.9	143	6	US-08-808-599A-41
5	40	50.6	345	1	Patent No. 5260432-3
6	40	50.6	345	1	Sequence 1, Appli
7	40	50.6	345	3	US-08-843-993-1
8	40	50.6	345	3	Sequence 1, Appli
9	40	50.6	413	2	US-09-059-520A-1
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14	39	49.4	126	5	Sequence 15, Appli
15	39	49.4	126	5	PCT-US96-03916-15
16	39	49.4	126	5	Sequence 4, Appli
17	39	49.4	126	5	US-08-276-151-4
18	39	49.4	126	5	US-08-866-751A-5
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20	39	49.4	126	5	US-08-676-166A-2
21	39	49.4	126	5	Sequence 2, Appli
22	39	49.4	126	5	Sequence 148, App
23	39	49.4	126	5	Sequence 148, App
24	39	49.4	126	5	US-08-897-438-148
25	39	49.4	126	5	Sequence 2, Appli
26	39	49.4	126	5	US-08-276-151-2
27	39	49.4	126	5	Sequence 1, Appli
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29	39	49.4	126	5	Sequence 3, Appli
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31	39	49.4	126	5	Sequence 5, Appli
32	39	49.4	126	5	Sequence 12, Appli
33	39	49.4	126	5	Sequence 6, Appli
34	39	49.4	126	5	Sequence 13, Appli
35	39	49.4	126	5	Sequence 1, Appli
36	39	49.4	126	5	Sequence 19, Appli
37	39	49.4	126	5	US-08-613-009A-19

28	39	49.4	660	1	US-08-487-890A-8	Sequence 8, Appli
29	39	49.4	660	1	US-08-487-890A-10	Sequence 10, Appli
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43	39	49.4	951	4	US-05-335-411-58	Sequence 58, Appli
44	39	49.4	952	2	US-08-788-674-5	Sequence 5, Appli
45	39	49.4	952	3	US-08-816-346-4	Sequence 4, Appli

#### ALIGNMENTS

RESULT 1  
US-08-187-793-4  
; Sequence 4, Application US/08187793  
; Patent No. 5614371  
; GENERAL INFORMATION:  
; APPLICANT: POSNER, JEROME B.  
; APPLICANT: DARNELL, ROBERT B.  
; APPLICANT: FURNEAUX, HENRY M.  
; TITLE OF INVENTION: ANTIGEN RECOGNIZED BY ANTIBODIES ASSOCIATED  
; TITLE OF INVENTION: WITH PARANEOPlastic OPsOCLONUS AND METHODS OF  
; TITLE OF INVENTION: USE THEREOF  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: COOPER & DUNHAM  
; STREET: 30 ROCKEFELLER PLAZA  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: U.S.A.  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/187,793  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 691,559  
; FILING DATE: 25-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WHITE, JOHN P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 39227  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 977-9550  
; TELEFAX: (212) 664-0525  
; TELEX: (212) 422523 COOP UI  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 530 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-187-793-4

Query Match 62.0%; Score 49; DB 1; Length 530;  
Best Local Similarity 58.8%; Pred. No. 5.3;

us-09-763-397a-22.ra1

Mon Feb 4 15:23:44 2002

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; REFERENCE/DOCKET NUMBER: P-LA 2256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-808-599A-41

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Db 1 PSSSTSPSSTSTSS 15

RESULT 4
5260432-3
; Patent No. 5260432
; APPLICANT: TAKAKU, FUMIMARO; ISHIKAWA, TAKASHI; IMAWARI, MICHIO;
; EVANS, RONALD M.; UMESONO, KAZUHIKO
; TITLE OF INVENTION: HUMAN GAMMA RETINOIC ACID RECEPTOR DNA
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/370,407
; FILING DATE: 22-JUN-1989
; SEQ ID NO: 3
; LENGTH: 143
; 5260432-3

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Best Local Similarity 72.7%; Pred. No. 19;
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Db 129 SSPSSNRSSPA 139

RESULT 5
US-08-843-993-1
; Sequence 1, Application US/08843993
; Patent No. 5739010
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN TRANSCRIPTION FACTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER, READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; APPLICATION NUMBER: US/08/843,993
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:

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Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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Db 176 SSPTTKSSPSDPMTWS 192

RESULT 2
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; Sequence 2, Application US/09300672
; Patent No. 6248937
; GENERAL INFORMATION:
; APPLICANT: Finkelstein, Ruth R.
; APPLICANT: Lynch, Tim
; APPLICANT: Goodman, Howard M.
; APPLICANT: Wang, Ming-Li
; TITLE OF INVENTION: A TRANSCRIPTION FACTOR REGULATING SEED DEVELOPMENT,
; TITLE OF INVENTION: QUALITY AND COLD-TOLERANCE
; FILE REFERENCE: 480.89(HV)
; CURRENT APPLICATION NUMBER: US/09/300,672
; CURRENT FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Arabidopsis
; US-09-300-672-2

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Best Local Similarity 64.7%; Pred. No. 4.4;
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Db 113 SSPSSVSSSSSSVSAS 129

RESULT 3
US-08-808-599A-41
; Sequence 41, Application US/08808599A
; Patent No. 6111089
; GENERAL INFORMATION:
; APPLICANT: Fukuda, Michiko N.
; TITLE OF INVENTION: Trophinin, Trophinin-Assisting
; TITLE OF INVENTION: Proteins and Methods to Inhibit Implantation
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER, READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; APPLICATION NUMBER: US/08/808,599A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/317,522
; FILING DATE: 04-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/439,818
; FILING DATE: 12-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815

```

NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0274 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 345 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: SYN00AT01  
CLONE: 727885  
US-08-843-993-1

Query Match 50.6%; Score 40; DB 1; Length 345;  
Best Local Similarity 52.9%; Pred. No. 75;  
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 SSPSTKSSPSNVKSAS 17  
DB 70 SSPSAGNSPSSLKFPS 86

RESULT 6  
US-09-059-520A-1  
; Sequence 1, Application US/09059520A  
; Patent No. 6001971  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: HUMAN TRANSCRIPTION FACTOR  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/059,520A  
; FILING DATE: Filed Herewith  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0274 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 345 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: SYN00AT01  
; CLONE: 727885  
US-09-059-520A-1

Query Match 50.6%; Score 40; DB 3; Length 345;  
Best Local Similarity 52.9%; Pred. No. 75;  
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 SSPSTKSSPSNVKSAS 17  
DB 70 SSPSAGNSPSSLKFPS 86

RESULT 7  
US-09-334-275-1  
; Sequence 1, Application US/09334275  
; Patent No. 6037132  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: HUMAN TRANSCRIPTION FACTOR  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/334,275  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/059,520  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0274 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 345 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: SYN00AT01  
; CLONE: 727885  
US-09-334-275-1

Query Match 50.6%; Score 40; DB 3; Length 345;  
Best Local Similarity 52.9%; Pred. No. 75;  
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 SSPSTKSSPSNVKSAS 17  
DB 70 SSPSAGNSPSSLKFPS 86

RESULT 8  
US-08-481-814A-8  
; Sequence 8, Application US/08481814A  
; Patent No. 5869040  
; GENERAL INFORMATION:  
; APPLICANT: Hsu, Yen-Ming  
; TITLE OF INVENTION: GENE THERAPY METHODS AND COMPOSITIONS  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:

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; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US-08/481,814A
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A
; REFERENCE/DOCKET NUMBER: A001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2000
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-481-814A-8
;
Query Match 50.6%; Score 40; DB 2; Length 413;
Best Local Similarity 58.8%; Pred. No. 92;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
;
QY 1 SSPSTKSSPSNVKSAS 17
Db 309 SSSSSSSSSSSNSNSSS 325
;
RESULT 9
US-08-836-582-2
; Sequence 2, Application US/08836582
; Patent No. 604599
; GENERAL INFORMATION:
; APPLICANT: Bernards, Rene
; APPLICANT: Beijersbergen, Roderick L
; TITLE OF INVENTION: Transcription factor E2F-4
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye
; STREET: 1100 No. 6045999th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,582
; FILING DATE: 10-Mar-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,582
; FILING DATE: <Unknown>
; APPLICATION NUMBER: GB 9423049.7
; FILING DATE: 15-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Arthur R. Crawford
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 620-18
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-265-566-2
;
Query Match 50.6%; Score 40; DB 4; Length 413;
Best Local Similarity 58.8%; Pred. No. 92;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
;
QY 1 SSPSTKSSPSNVKSAS 17
Db 309 SSSSSSSSSSSNSNSSS 325
;
RESULT 10
US-09-265-566-2
; Sequence 2, Application US/09265566
; Patent No. 6303335
; GENERAL INFORMATION:
; APPLICANT: Bernards, Rene
; APPLICANT: Beijersbergen, Roderick L
; TITLE OF INVENTION: Transcription factor E2F-4
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye
; STREET: 1100 No. 6303335th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/265,566
; FILING DATE: 10-Mar-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,582
; FILING DATE: <Unknown>
; APPLICATION NUMBER: GB 9423049.7
; FILING DATE: 15-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Arthur R. Crawford
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 620-18
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-265-566-2
;
Query Match 50.6%; Score 40; DB 4; Length 413;
Best Local Similarity 58.8%; Pred. No. 92;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
;
QY 1 SSPSTKSSPSNVKSAS 17

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Db 309 SSSSSSSSSSSNSSS 325

## RESULT 11

PCT-US96-03916-15  
; Sequence 15, Application PC/TUS9603916  
; GENERAL INFORMATION:  
; APPLICANT: Wild, Martha A.  
; APPLICANT: Cochran, Mark D.  
; TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS  
; TITLE OF INVENTION: AND USES THEREOF  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/03916  
; FILING DATE: 23-MAR-1995  
; CLASSIFICATION:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/126,597  
; FILING DATE: 24-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 39116-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 126 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US96-03916-15

Query Match 49.4%; Score 39; DB 5; Length 126;  
Best Local Similarity 61.5%; Pred. No. 34;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SPSSTKSSPSNVK 14

Db 10 SPSDHASSPANAK 22

RESULT 12

US-08-276-151-4  
; Sequence 4, Application US/08276151  
; Patent No. 5597719  
; GENERAL INFORMATION:  
; APPLICANT: Freed, Ellen  
; APPLICANT: Ruggieri, Rosamaria  
; TITLE OF INVENTION: Interaction of raf-1 and 14-3-3 Proteins  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooley Godward et al.  
; STREET: Five Palo Alto Square  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94036  
; COMPUTER READABLE FORM:

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/886,751A  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Young, Leona G.  
; REGISTRATION NUMBER: 37,266  
; REFERENCE/DOCKET NUMBER: 25490-0100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 818-3700  
; TELEFAX: (404) 818-3799  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 217 amino acids

Qy 1 SPSSTKSSPSNV 13

Db 103 ASPSALSSPNL 115

RESULT 13

US-08-886-751A-5  
; Sequence 5, Application US/08886751A  
; Patent No. 5885783  
; GENERAL INFORMATION:  
; APPLICANT: Yoo, Tai-June  
; APPLICANT: Cheng, Kuang-Chuan  
; TITLE OF INVENTION: Autoimmune Inner Ear Disease Antigen and  
; TITLE OF INVENTION: Diagnostic Assay  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jones & Askew  
; STREET: 191 Peachtree Street, 37th Floor  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: U.S.A.  
; ZIP: 30303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/886,751A  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Young, Leona G.  
; REGISTRATION NUMBER: 37,266  
; REFERENCE/DOCKET NUMBER: 25490-0100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 818-3700  
; TELEFAX: (404) 818-3799  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 217 amino acids

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/886,751A  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Young, Leona G.  
; REGISTRATION NUMBER: 37,266  
; REFERENCE/DOCKET NUMBER: 25490-0100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 818-3700  
; TELEFAX: (404) 818-3799  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 217 amino acids

Qy 1 SPSSTKSSPSNV 13

Db 103 ASPSALSSPNL 115

RESULT 13

US-08-886-751A-5  
; Sequence 5, Application US/08886751A  
; Patent No. 5885783  
; GENERAL INFORMATION:  
; APPLICANT: Yoo, Tai-June  
; APPLICANT: Cheng, Kuang-Chuan  
; TITLE OF INVENTION: Autoimmune Inner Ear Disease Antigen and  
; TITLE OF INVENTION: Diagnostic Assay  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jones & Askew  
; STREET: 191 Peachtree Street, 37th Floor  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: U.S.A.  
; ZIP: 30303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/886,751A  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Young, Leona G.  
; REGISTRATION NUMBER: 37,266  
; REFERENCE/DOCKET NUMBER: 25490-0100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 818-3700  
; TELEFAX: (404) 818-3799  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 217 amino acids

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/886,751A  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Young, Leona G.  
; REGISTRATION NUMBER: 37,266  
; REFERENCE/DOCKET NUMBER: 25490-0100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 818-3700  
; TELEFAX: (404) 818-3799  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 217 amino acids





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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 10:26:50 ; Search time 34.94 seconds  
(without alignments)  
37.063 Million cell updates/sec

Title: US-09-763-397A-22

Perfect score: 79  
Sequence: 1 SSPSSTKSSPSNVKSAS 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68.\*

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68.5	86.7	782	2 S27833	rhostry-associated
2	49	62.0	510	2 I38489	onconeural ventral
3	48	60.8	328	2 G84826	hypothetical prote
4	48	60.8	725	2 A41258	a-agglutinin core
5	48	60.8	1446	1 A45344	immediate-early pr
6	47	59.5	497	2 E82537	hypothetical prote
7	47	59.5	515	2 A25048	regulatory protein
8	46	58.2	244	2 T12458	hypothetical prote
9	45	57.0	211	2 D96507	hypothetical prote
10	45	57.0	349	2 T41394	hypothetical serin
11	45	57.0	626	2 JC5405	brain and muscle A
12	45	57.0	626	2 JE0270	Ant-like PAS prot
13	45	57.0	2559	2 T09144	probable guanine n
14	44	55.7	214	2 T51657	myb-related transc
15	44	55.7	229	2 T04764	hypothetical prote
16	44	55.7	267	2 H86320	probable MYB47 tra
17	44	55.7	892	2 A41697	nitrate assimilati
18	44	55.7	928	2 T24868	hypothetical prote
19	44	55.7	1194	2 E96624	hypothetical prote
20	43	54.4	230	2 D86352	protein T26F17.14
21	43	54.4	230	2 T39598	hypothetical serin
22	43	54.4	327	2 G01037	T-cell activation
23	43	54.4	388	2 S04783	protoporphyrin
24	43	54.4	402	2 E86185	hypothetical prote
25	43	54.4	448	2 B56558	retinoic acid rece
26	43	54.4	541	2 D84681	hypothetical prote
27	43	54.4	542	2 T06728	pectate lyase [EC
28	43	54.4	701	2 T52384	hypothetical prote
29	43	54.4	969	2 F71418	hypothetical prote

30	54.4	1032	2 T34433	hypothetical prote	
31	43	54.4	2 A59235	unconventional myo	
32	43	1807	2 S03124	vitellogenin A2 pr	
33	43	54.4	2 T34434	hypothetical prote	
34	42.5	53.8	1 EDBE1F	immediate-early pr	
35	42	53.2	2 T39869	probable lysophosp	
36	42	53.2	380	2 T01281	probable leucine-r
37	42	53.2	453	2 T50674	retinoic acid rece
38	42	53.2	459	2 A41977	retinoic acid rece
39	42	53.2	464	2 A56558	retinoic acid rece
40	42	53.2	496	2 T01584	hypothetical prote
41	42	53.2	503	2 S63257	probable membrane
42	42	53.2	507	2 S64507	serine-rich protei
43	42	53.2	534	2 T39903	related to BCS1 pr
44	42	53.2	779	2 T49717	hypothetical prote
45	42	53.2	796	2 T21460	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

S27833  
rhostry-associated protein 1 precursor - malaria parasite (Plasmodium falciparum)  
N:Alternate names: protective antigen  
C:Species: Plasmodium falciparum  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jun-2000  
C:Accession: A45514; S27833  
R:Ridley, R.G.; Takacs, B.; Lahm, H.W.; Delves, C.J.; Coman, M.; Certa, U.; Matile, H  
Mol. Biochem. Parasitol. 41, 125-134, 1990  
A:Title: Characterisation and sequence of a protective rhostry antigen from Plasmodiu  
A:Reference number: A45514; MUID:90348711  
A:Accession: A45514  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-782 <R12>  
A:Cross-references: GB:M32853; NID:g160656; PID:g160657  
C:Superfamily: Plasmodium falciparum rhostry-associated protein 1

Query Match 86.7%; Score 68.5; DB 2; Length 782;  
Best Local Similarity 94.4%; Pred. No. 0.014;  
Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SSPSSTK-SSPSNVKSAS 17  
||||| |||||||  
Db 145 SSPSSTKSSPSNVKSAS 162

##### RESULT 2

I38489  
onconeural ventral antigen-1 - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 05-Nov-1999  
C:Accession: I38489  
R:Buckanovich, R.J.; Posner, J.B.; Darnell, R.B.  
Neuron 11, 657-672, 1993  
A:Title: Nova, the Paraneoplastic Ri Antigen, is Homologous to an RNA-Binding Protein  
A:Reference number: I38489; MUID:94000830  
A:Accession: I38489  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-510 <RES>  
A:Cross-references: EMBL:U04840; NID:g440877; PIDN:AAA16022.1; PID:g440878  
C:Genetics:  
A:Gene: Nova-1

Query Match 62.0%; Score 49; DB 2; Length 510;  
Best Local Similarity 58.8%; Pred. No. 7.3;  
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SSPSSTKSSPSNVKSAS 17



## RESULT 7

A25048  
regulatory protein STE7 - yeast (Saccharomyces cerevisiae)  
N:Alternate names: protein D1525; protein YDL159w  
C:Species: Saccharomyces cerevisiae  
C>Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 24-Sep-1999  
C:Accession: A25048; S61054; S67711; S67707  
R:Teague, M.A.; Chaleff, D.T.; Errede, B.  
Proc. Natl. Acad. Sci. U.S.A. 83, 7371-7375, 1986  
A:Title: Nucleotide sequence of the yeast regulatory gene STE7 predicts a protein homologous to the protein kinase homology domain of the yeast regulatory gene STE7  
A:Reference number: A25048; MUID:87016949  
A:Accession: A25048  
A:Molecule type: DNA  
A:Residues: 1-515 <TEA>  
A:Cross-references: EMBL:M14097; NID:g172761; PIDN:AAA35118.1; PID:g172762  
R:Pohl, T.M.  
submitted to the EMBL Data Library, November 1995  
A:Reference number: S61010  
A:Accession: S61054  
A:Molecule type: DNA  
A:Residues: 1-515 <POH>  
A:Cross-references: EMBL:Z67750; NID:g1061256; PIDN:CAA91587.1; PID:g1061280  
R:Pohl, T.M.  
submitted to the Protein Sequence Database, July 1996  
A:Reference number: S67708  
A:Accession: S67711  
A:Molecule type: DNA  
A:Residues: 1-515 <POW>  
A:Cross-references: EMBL:Z74207; NID:g1431250; PIDN:CAA98732.1; PID:e253067; PID:g143125  
A:Experimental source: strain S288C  
R:Perea, J.; Blugeon, C.; Delaveau, T.; Jacq, C.  
submitted to the Protein Sequence Database, July 1996  
A:Reference number: S67693  
A:Accession: S67707  
A:Molecule type: DNA  
A:Residues: 71-515 <PER>  
A:Cross-references: EMBL:Z74207; MIPS:YDL159w  
A:Experimental source: strain S288C  
C:Genetics:  
A:Gene: SGD:STE7  
A:Cross-references: SGD:S0002318; MIPS:YDL159w  
A:Map position: 4L  
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology  
C:Keywords: ATP; phosphoprotein; serine/threonine-specific protein kinase  
F:189-466/Domain: protein kinase homology <KIN>  
F:197-205/Region: protein kinase ATP-binding motif

Query Match 59.5%; Score 47; DB 2; Length 515;  
Best Local Similarity 56.2%; Pred. No. 15;  
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 SPSSTKSSPSNVKAS 17  
|||||I:|:|:|  
DB 130 SPSSTNSTPSTIGLS 145

## RESULT 8

T12458  
hypothetical protein DKFzp56400823.1 - human  
C:Species: Homo sapiens (man)  
C>Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 23-Jul-1999  
C:Accession: T12458  
R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, June 1999  
A:Reference number: Z17524  
A:Accession: T12458  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-244 <WAM>  
A:Cross-references: EMBL:AL080121

A:Experimental source: fetal brain; clone DKFzp56400823  
C:Genetics:  
A:Note: DKFzp56400823.1

Query Match 58.2%; Score 46; DB 2; Length 244;  
Best Local Similarity 64.7%; Pred. No. 9.8;  
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 SSPSSTKSSPSNVKAS 17  
|||||I:|:|:|

DB 156 SSPSSLSTSPPEVFSAS 172  
|||||I:|:|:|

## RESULT 9

D96507  
hypothetical protein T12C22.10 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: D96507  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marzia  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719  
A:Accession: D96507  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-211 <STO>  
A:Cross-references: GB:AE005173; NID:g8655993; PIDN:AAF78266.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: T12C22.10  
A:Map position: 1

Query Match 57.0%; Score 45; DB 2; Length 211;  
Best Local Similarity 58.8%; Pred. No. 12;  
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 SSPSSTKSSPSNVKAS 17  
|||||I:|:|:|  
DB 13 SSPSSSSSSSTSSSS 29

## RESULT 10

T41394  
hypothetical serine-rich protein - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C:Accession: T41394  
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.  
submitted to the EMBL Data Library, May 1998  
A:Reference number: Z21991  
A:Accession: T41394  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-349 <WOO>  
A:Cross-references: EMBL:AL023704; PIDN:CAA19262.1; GSPDB:GN00068; SPDB:SPCC553.10  
A:Experimental source: strain 972h-; cosmid C553  
C:Genetics:  
A:Gene: SPDB:SPCC553.10  
A:Map position: 3

Query Match 57.0%; Score 45; DB 2; Length 349;  
Best Local Similarity 64.7%; Pred. No. 20;  
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;





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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 29, 2002, 11:13:51 ; Search time 20.36 seconds  
(without alignments)  
30.614 Million cell updates/sec

Title: US-09-763-397A-22

Perfect score: 79

Sequence: 1 SSPSSTKSSPSNVKSAS 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	49	62.0	510	1 NOAL_HUMAN	P51513 homo sapien
2	48	60.8	725	1 AGAL_YEAST	RP P32323 saccharomyc
3	48	60.8	1446	1 IE18_PRVKA	RC P33479 pseudorabie
4	47	59.5	515	1 STE7_YEAST	RC P06784 saccharomyc
5	46	58.2	710	1 IRAL_MOUSE	O62406 mus musculu
6	45	57.0	583	1 BMAL_HUMAN	RL O00327 homo sapien
7	44	55.7	234	1 RACD_DICDI	P34150 dictyostell
8	44	55.7	892	1 NIRA_EMENI	RP28348 emerice
9	43	54.4	388	1 PORA_HORVU	PL13653 hordeum vul
10	43	54.4	583	1 API_KLULA	P56095 kluyveromyc
11	43	54.4	681	1 BRC2_HALRO	O01409 halocynthia
12	43	54.4	1807	1 VTA2_XENLA	PL18709 xenopus lae
13	42.5	53.8	1461	1 IE18_PRVIF	PL1675 pseudorabie
14	42	53.2	458	1 RRA_XENLA	P51126 xenopus lae
15	42	53.2	503	1 YN23_YEAST	P53832 saccharomyc
16	42	53.2	507	1 YG46_YEAST	P53301 saccharomyc
17	42	53.2	796	1 YS8A_CAEEL	O09625 caenorhabdi
18	42	53.2	845	1 CLPC_CHLPN	Q92866 chlamydia p
19	42	53.2	1214	1 SIPI_HUMAN	O60315 homo sapien
20	42	53.2	1215	1 SIPI_MOUSE	Q90977 mus musculu
21	42	53.2	1475	1 N153_HUMAN	P49790 homo sapien
22	42	53.2	1627	1 TP2B_CHICK	O42131 gallus gall
23	42	53.2	1850	1 VIT2_CHICK	P02845 gallus gall
24	41	51.9	485	1 Y136_TREPA	O83172 treponema p
25	41	51.9	561	1 CP51_USTMA	P49602 ustilago ma
26	41	51.9	1071	1 SEFI_KLULA	RP87164 kluyveromyc
27	41	51.9	1091	1 NCAL_CHICK	PL13590 gallus gall
28	41	51.9	1147	1 AC15_HUMAN	P35251 homo sapien
29	41	51.9	1597	1 RLRI_YEAST	P53552 saccharomyc
30	41	51.9	1992	1 TR12_HUMAN	Q14669 homo sapien
31	40.5	51.3	483	1 ODP2_SCHPO	O59816 schizosacch
32	40	50.6	161	1 19KD_MYCAV	P46733 mycobacteri
33	40	50.6	304	1 CAH5_RAT	P43165 rattus norv

#### ALIGNMENTS

RESULT 1

ID	NOAL_HUMAN	STANDARD;	PRT;	510 AA.
AC	P51513:			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	ONCONEURAL VENTRAL ANTIGEN-1 (NOVA-1) (PARANEOPLASTIC RI ANTIGEN)			
DE	(VENTRAL NEURON-SPECIFIC PROTEIN 1).			
GN	NOVA1			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Cerebellum, and Hippocampus;			
RX	MEDLINE=94000830; PubMed=8398153;			
RA	Buckanovich R.J., Posner J.B., Darnell R.B.;			
RT	"Nova, the paraneoplastic RI antigen, is homologous to an RNA-binding			
RT	protein and is specifically expressed in the developing motor			
RT	system."			
RL	Neuron 11:657-672(1993).			
RN	[2]			
RP	SEQUENCE OF 1-34 FROM N.A.			
RC	TISSUE=Fetal brain;			
RA	Dmitrenko V.V., Garifulin O.M., Shostak K.A., Smikodub A.I.,			
RA	Kavsan V.M.;			
RP	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: MAY REGULATE RNA SPLICING OR METABOLISM IN A SPECIFIC			
CC	SUBSET OF DEVELOPING NEURONS.			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR.			
CC	-1- TISSUE SPECIFICITY: BRAIN.			
CC	-1- DISEASE: ANTIBODIES ARE SEEN AGAINST THIS ANTIGEN IN THE PATIENTS			
CC	SUFFERING WITH PARANEOPLASTIC OPSOCLONUS-ATAXIA (POA). POA IS A			
CC	DISORDER IN WHICH ABNORMAL MOTOR CONTROL OF THE EYES, TRUNK AND			
CC	LIMBS DEVELOP IN WOMEN WITH BREAST OR SMALL LUNG CANCER. POA			
CC	PATIENTS SUFFER FROM OPSOCLONUS, A CHAOTIC EYE MOVEMENT DISORDER			
CC	ATTRIBUTABLE TO A LACK OF INHIBITION OF BURST NEURONS IN THE BRAIN			
CC	STEM; MYOCLONUS, A DISORDER PERHAPS ATTRIBUTING TO A FAILURE OF			
CC	INHIBITORY CONTROL OVER SPINAL MOTOR NEURONS; AND TRUNCAL ATAXIA,			
CC	REFERABLE TO CEREBELLAR DYSFUNCTION; THERE ARE NO CORTICAL OR			
CC	SENSORY DEFICITS.			
CC	-1- SIMILARITY: CONTAINS 3 KH DOMAINS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL; U04840; AAA16022.1; -			
DR	EMBL; Z70771; CAA94810.1; -			
DR	MM; 602157; -			

34	40	50.6	345	1	KLF3_HUMAN	P57682 homo sapien
35	40	50.6	355	1	YP11_YEAST	P48559 saccharomyc
36	40	50.6	372	1	COQ2_YEAST	P32378 saccharomyc
37	40	50.6	376	1	MID2_YEAST	P36027 saccharomyc
38	40	50.6	413	1	E2F4_HUMAN	Q16254 homo sapien
39	40	50.6	417	1	MAC1_YEAST	P35192 saccharomyc
40	40	50.6	702	1	YAI4_YEAST	P27637 saccharomyc
41	40	50.6	709	1	SYR_CAEEL	Q19825 caenorhabdi
42	40	50.6	743	1	YCR6_YEAST	P25353 saccharomyc
43	40	50.6	754	1	UBP9_YEAST	P39967 saccharomyc
44	40	50.6	823	1	YRR2_CAEEL	Q09345 caenorhabdi
45	40	50.6	888	1	STU2_YEAST	P46675 saccharomyc

DR InterPro: IPR000958; KH.  
DR Pfam: PF00013; KH-domain; 3.  
DR SMART: SM00322; KH; 3.  
DR PROSITE: PS50084; KH\_TYPE\_1; 3.  
KW Nuclear protein; RNA-binding; Repeat; Alternative splicing; Antigen.  
FT DOMAIN 52 87  
FT DOMAIN 177 212 KH 1.  
FT DOMAIN 427 462 KH 2.  
FT DOMAIN 427 462 KH 3.  
FT VARSPLIC 88 90 MISSING (IN TUMOR ISOFORM).  
FT VARSPLIC 153 176 MISSING (IN ISOFORM 3).  
FT VARSPLIC 177 184 VKIVPNS -> KHNISWIS (IN TUMOR ISOFORM).  
FT VARSPLIC 185 510 MISSING (IN TUMOR ISOFORM).  
SQ SEQUENCE 510 AA; 52055 MW; 7B9BA8B67CAB6984 CRC64.

Query Match 62.0%; Score 49; DB 1; Length 510;  
Best Local Similarity 58.8%; Pred. No. 3.9;  
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SSPSTKSPSPNVKAS 17  
|||||:||||: :|  
Db 156 SSPTTKSPSPDPMTS 172

RESULT 2  
AGAL\_YEAST  
ID AGAL\_YEAST STANDARD; PRT; 725 AA.  
AC P32323;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DE 01-OCT-1996 (Rel. 34, Last annotation update)  
DE A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.  
GN AGAL OR YNR044W OR N3431.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pohl T.M.;  
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: MEDIATES THE CELL SURFACE ATTACHMENT OF THE A-AGGLUTININ  
CC SUBUNIT. S. CEREVISIAE A AND ALPHA CELLS EXPRESS THE COMPLEMENTARY  
CC CELL SURFACE GLYCOPROTEINS A-AGGLUTININ AND ALPHA-AGGLUTININ,  
CC RESPECTIVELY, WHICH INTERACT WITH ONE ANOTHER TO PROMOTE CELLULAR  
CC AGGREGATION DURING MATING.  
CC -1- SUBUNIT: CONTAINS AT LEAST A BINDING SUBUNIT DISULFIDE-LINKED TO  
CC A CORE SUBUNIT.  
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR  
CC AND/OR BY CARBOHYDRATE-MEDIATED COVALENT CROSS-LINKS (POSSIBLE).  
CC -1- PTM: EXTENSIVELY O-GLYCOSYLATED.  
CC  
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DR EMBL; M60590; AAA34382.1; -;  
DR EMBL; Z71659; CAA96325.1; -;  
DR PIR; S17031; S17031.  
DR PIR; A41258; A41258.  
DR SGD; S0005327; AGAL.  
KW Glycoprotein; Cell adhesion; Signal; GPI-anchor; Repeat;

KW Pheromone response.  
FT SIGNAL 1 22  
FT CHAIN 23 725  
FT DOMAIN 53 493  
FT REPEAT 53 149  
FT REPEAT 395 493  
FT DOMAIN 182 307  
FT REPEAT 182 188  
FT REPEAT 189 195  
FT REPEAT 196 202  
FT REPEAT 203 209  
FT REPEAT 210 216  
FT REPEAT 217 223  
FT REPEAT 224 230  
FT REPEAT 231 237  
FT REPEAT 238 244  
FT REPEAT 245 251  
FT REPEAT 252 258  
FT REPEAT 259 265  
FT REPEAT 266 272  
FT REPEAT 273 279  
FT REPEAT 280 286  
FT REPEAT 287 293  
FT REPEAT 294 300  
FT REPEAT 301 307  
SQ SEQUENCE 725 AA; 73353 MW; 70420C853B0B01F8 CRC64;

Query Match 60.8%; Score 48; DB 1; Length 725;  
Best Local Similarity 52.9%; Pred. No. 7.9;  
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SSPSTKSPSPNVKAS 17  
|||||:||||: :|  
Db 191 TSPSTSTSPSTSTSS 207

RESULT 3  
IE18\_PRVKA  
ID IE18\_PRVKA STANDARD; PRT; 1446 AA.  
AC P33479; 1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last annotation update)  
DE IMMEDIATE-EARLY PROTEIN IE180.  
GN IE.  
OS Pseudorabies virus (strain Kaplan) (PRV).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Varicellovirus.  
OX NCBI\_TaxID=33703;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91021039; PubMed=2171211;  
RA Vicek C., Kozmik Z., Paces V., Schirm S., Schwyzer M.;  
RT "Pseudorabies virus immediate-early gene overlaps with an oppositely  
RT oriented open reading frame: characterization of their promoter and  
RT enhancer regions."  
RL Virology 179:365-377(1990).  
CC -1- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE  
CC OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING  
CC OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.  
CC -1- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.  
CC -1- PTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF  
CC PHOSPHORYLATION.  
CC -1- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.  
CC  
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CC -1- PATHWAY : RESPONSE TO PHEROMONE-INDUCED SIGNAL.  
CC -1- SIMILARITY : BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC MAP KINASE KINASE SUBFAMILY.  
CC -----  
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CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL; M14097; AAA35118.1; -;  
CC DR EMBL; Z67750; CAA91587.1; -;  
CC DR EMBL; Z74207; CAA98732.1; -;  
CC DR EMBL; X97751; CAA66332.1; -;  
CC DR PIR; A25048; A25048.  
CC DR SGD; S0002318; STE7.  
CC DR InterPro; IPR000719; Euk\_pkinase.  
CC DR InterPro; IPR002290; Ser\_thr\_kin\_actsite.  
CC DR Pfam; PF00069; pkinase; 1.  
CC DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
CC DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
CC DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
CC DR Transferrase; Serine/threonine-protein kinase; ATP-binding;  
CC KW Phosphorylation; Pheromone response.  
CC FT DOMAIN 191 466 PROTEIN KINASE.  
CC FT NP\_BIND 197 205 ATP (BY SIMILARITY).  
CC FT BLINDING 220 220 ATP (BY SIMILARITY).  
CC FT ACT\_SITE 331 331 BY SIMILARITY.  
CC FT MOD\_RES 359 359 PHOSPHORYLATION.  
CC FT MOD\_RES 363 363 PHOSPHORYLATION.  
CC FT MUTAGEN 353 353 S->A: NO LOSS OF ACTIVITY.  
CC FT MUTAGEN 359 359 S->A: INACTIVATION.  
CC FT MUTAGEN 363 363 T->A: INACTIVATION.  
CC SQ SEQUENCE 515 AA; 57709 MW; G8A75899CFBE8BDE CRC64;

Query Match 59.5%; Score 47; DB 1; Length 515;  
Best Local Similarity 56.2%; Pred.No. 7.7; Indels 0; Gaps 0;  
Matches 9; Conservative 3; Mismatches 4

Qy 2 SPSTKSSPSNVKSAS 17  
Db 130 SPSTNSTPTSIQGLS 145  
|||||:|||::|

RESULT 5  
IRAL\_MOUSE STANDARD; PRT; 710 AA.  
ID IRAL\_MOUSE  
AC Q62406; 20-AUG-2001 (Rel. 40, Created)  
DT 20-AUG-2001 (Rel. 40, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE INTERLEUKIN-1 RECEPTOR-ASSOCIATED KINASE 1 (EC 2.7.1.-) (IRAK-1)  
DE (IRAK) (PELLE-LIKE PROTEIN KINASE) (MPLK).  
GN IRAK1 OR ILIRAK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OC NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kopp E.B., Ghosh S.;  
RL "Cloning of mouse IRAK.";  
RT Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.  
[2]  
RN RP SEQUENCE FROM N.A.  
RA Harrington M.A.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.  
[3]  
RN RP SEQUENCE OF 34-710 FROM N.A.  
RC TISSUE=Embryo;

RX MEDLINE-96279287; PubMed-8663605;  
RA Trolimova M., Sprengle A.B., Green M., Sturgill T.W., Goebel M.G.,  
RA Harrington M.A.,  
RT "developmental and tissue-specific expression of mouse pelle-like  
RT protein kinase.";  
RL J. Biol. Chem. 271:17609-17612(1996).  
CC -1- FUNCTION: INVOLVED IN IL-1 PATHWAY. THIS KINASE ASSOCIATES WITH  
CC THE IL-1 RECEPTOR IL1-R-1. THIS ASSOCIATION IS RAPID AND IL-1  
CC DEPENDENT (BY SIMILARITY).  
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LIVER, FOLLOWED BY KIDNEY  
CC AND SKELETAL MUSCLE.  
CC -1- DEVELOPMENTAL STAGE: EXPRESSED FROM E11 DAY TO E18 DAY.  
CC -1- PTM: AUTOPHOSPHORYLATED. AN EXTENSIVE PHOSPHORYLATION OF IRAK  
CC OCCURS AFTER ITS ASSOCIATION WITH IL1-R-1. THIS STEP COULD BE  
CC LINKED TO THE ACTIVATION OF THE KINASE (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC PELLE SUBFAMILY.  
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CC -----  
DR EMBL; U56773; AAC52694.2; -;  
DR EMBL; AF103876; AAD13224.1; ALT\_INIT.  
DR MGD; MGI:107420; Il1rak.  
DR InterPro; IPR000719; Euk\_pkinase.  
DR InterPro; IPR002290; Ser\_thr\_kin\_actsite.  
DR Pfam; PF00069; pkinase; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
DR PROSITE; PS50011; PROTEIN KINASE\_DOM; 1.  
KW Transferase; Serine/threonine-protein kinase; ATP-binding.  
FT DOMAIN 212 521 PROTEIN KINASE.  
FT NF\_BIND 218 226 ATP (BY SIMILARITY).  
FT BINDING 239 239 ATP (BY SIMILARITY).  
FT ACT\_SITE 338 338 BY SIMILARITY.  
SQ SEQUENCE 710 AA; 77269 MW; 8A501F002CD3EBD2 CRC64;  
  
Query Match 58.2%; Score 46; DB 1; Length 710;  
Best Local Similarity 75.0%; Pred. NO. 15;  
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
Oy 1 SPSSTKSPSN 12  
|:|||||||:  
Db 174 SAPSSTKSPES 185  
  
RESULT 6  
ID BMAL\_HUMAN STANDARD; PRT; 583 AA.  
AC O00327; O00313; O00314; O00315; O00316; O00317; Q99631; Q99649;  
DT 15-DEC-1998 (Rel. 37, Created)  
DR 13-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE BMALI PROTEIN (BRAIN AND MUSCLE ARNT-LIKE 1) (MEMBER OF PAS PROTEIN 3)  
DE (MOP3) (BHLH-PAS PROTEIN JAP3).  
GN BMALI OR ARNTL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS BMALI A-F).  
RC TISSUE=Brain;  
PX MEDLINE-97289529; PubMed-9144434;  
RA Ikeda M., Nomura M.;  
RT "cDNA cloning and tissue-specific expression of a novel basic  
RT helix-loop-helix/PAS protein (BMALI) and identification of

alternatively spliced variants with alternative translation  
RT initiation site usage.";  
RL Biochem. Biophys. Res. Commun. 233:258-264(1997).  
RN [2].  
RP SEQUENCE FROM N.A. (ISOFORM MOP3).  
RC TISSUE=Fetal brain;  
RX MEDLINE-97236817; PubMed-9079689;  
RA Hogenesch J.B., Chan W.K., Jackiw V.H., Brown R.C., Gu Y.-Z.,  
RA Pray-Grant M., Bradfield C.A.;  
RT "Characterization of a subset of the basic-helix-loop-helix-PAS  
RT superfamily that interacts with components of the dioxin signaling  
RT pathway.";  
RL J. Biol. Chem. 272:8581-8593(1997).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM BMALI1B).  
RA Tian H., Russell D.W., McKnight S.L.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP INTERACTION WITH CLOCK.  
RX MEDLINE-98279137; PubMed-9616112;  
RA Gekakis N., Strakos D., Nguyen H.B., Davis F.C., Wilsbacher L.D.,  
RA King D.P., Takahashi J.S., Weitz C.J.;  
RT "Role of the clock protein in the mammalian circadian mechanism.";  
RL Science 280:1564-1569(1998).  
CC -1- FUNCTION: CLOCK-BMALI HETERODIMERS BIND TO AN E-BOX ELEMENT (3'-  
CACGTG-5'), THEREBY ACTIVATING TRANSCRIPTION OF PER1, AND POSSIBLY  
CC OF OTHER CIRCADIAN CLOCK PROTEINS.  
CC -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER  
CC BHLH PROTEIN. FORMS AN HETERODIMER WITH CLOCK. INTERACTS WITH  
CC HSP90; WITH AHR IN VITRO, BUT NOT IN VIVO.  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).  
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 7 ISOFORMS; BMALI1 (SHOWN HERE),  
CC BMALI1/JAP3, BMALI1C, BMALI1D, BMALI1E, BMALI1F AND MOP3; ARE PRODUCED  
CC BY ALTERNATIVE SPLICING.  
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE ADULT BRAIN, SKELETAL  
CC MUSCLE AND HEART.  
CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF  
CC TRANSCRIPTION FACTORS. HOMOLOG OF DROSOPHILA CYCLE PROTEIN.  
CC -1- SIMILARITY: CONTAINS 1 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN.  
CC -----  
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CC -----  
DR EMBL; D89722; BAA19968.1; -;  
DR EMBL; AB000812; BAA19935.1; -;  
DR EMBL; AB000813; BAA19936.1; -;  
DR EMBL; AB000814; BAA19937.1; -;  
DR EMBL; AB000815; BAA19938.1; -;  
DR EMBL; AB000816; BAA19939.1; -;  
DR EMBL; U51627; AAC51213.1; -;  
DR EMBL; U60415; AAB37248.1; -;  
DR MIM; 602550;  
DR InterPro; IPR003015; HLH\_MYC.  
DR InterPro; IPR001092; HLH\_dlm.  
DR InterPro; IPR001067; Nucleoslocatr.  
DR InterPro; IPR001610; PAC.  
DR InterPro; IPR000014; PAC.  
DR Pfam; PF00010; HLH; 1.  
DR Pfam; PF00785; PAC; 1.  
DR Pfam; PF00989; PAS; 2.  
DR PRINTS; PR00785; NCTRNLOCATR.  
DR SMART; SM00353; HLH; 1.  
DR SMART; SM00086; PAC; 1.  
DR SMART; SM00091; PAS; 2.  
DR PROSITE; PS00038; HELIX\_LOOP\_HELIX; 1.  
KW Repeat; DNA-binding; Nuclear protein; Transcription regulation;  
KW Alternative splicing  
FT DNA\_BIND 30 42 BASIC DOMAIN.

FT DOMAIN 43 83  
FT REPEAT 103 170  
FT REPEAT 285 351  
FT REPEAT 358 401  
FT VARSPLIC 1 4  
FT VARSPLIC 1 16  
FT VARSPLIC 181 181  
FT VARSPLIC 182 583  
FT VARSPLIC 231 348  
FT VARSPLIC 235 258  
FT VARSPLIC 259 583  
FT VARSPLIC 400 483  
FT VARSPLIC 484 583  
FT CONFLICT 26 26  
FT CONFLICT 80 80  
FT CONFLICT 130 130  
FT CONFLICT 216 216  
FT CONFLICT 221 221  
FT CONFLICT 375 375  
FT CONFLICT 470 471  
FT CONFLICT 583 AA; 64206 MW; 2AABE7EB4A71119 CRC64;  
SQ SEQUENCE 583 AA; 64206 MW; 2AABE7EB4A71119 CRC64;

HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).  
PAS-1.  
PAS-2.  
PAC MOTIF.  
MINI -> MADORDISSITISDFMSPGPTDLLSSSLGTSGV  
DCNRKRKGSSTDYQ (IN ISOFORM BMALIB).  
MINIESMDTDKDDPHG -> MSKEAVSLMALTVSLQPPVPL  
CVCREMTGSGRRQCCVTLFFISRELCFYLLLEPPP (IN ISOFORM MOP3).  
T -> R (IN ISOFORM BMALIC).  
MISSING (IN ISOFORM BMALIC).  
MISSING (IN ISOFORM BMALID).  
SFTIHTSGYLSWPPKMGLED -> APTCTHSTGYGFI  
FTFRTSRHVL (IN ISOFORM BMALIE).  
MISSING (IN ISOFORM BMALIE).  
ANYLEGGDPTFPOLTAASHMSDMLSPSGGPKRTHPTVPG  
IPGGTRAGAGKIGMIAEIMEIHRGSSPSSCGSPLNI  
TS -> SRVDTGHLQVCTVLSRNSRFLIAGMETEPTS  
WRAGTQPSHSSQHPTAWTACCPLEKVAQRGPTPLFGFOG  
EPGLQGEK (IN ISOFORM BMALIF).  
MISSING (IN ISOFORM BMALIF).  
R -> G (IN REF. 2).  
K -> R (IN AB000812).  
S -> P (IN AB000816).  
K -> N (IN AB000815).  
D -> N (IN AB000815).  
S -> N (IN AB000814).  
SP -> LR (IN REF. 2).

Query Match 57.0%; Score 45; DB 1; Length 583;  
Best Local Similarity 66.7%; Pred. No. 17;  
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SSPSSTKSSPSNVKS 15  
||||| ||| | :  
DB 469 SSPSGSGSPLNITS 483

RESULT 7  
RACD\_DICDI  
ID RACD\_DICDI STANDARD; PRT; 254 AA.  
AC P34150; Q9GPS8;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 20-AUG-2001 (Rel. 40, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE RAS-RELATED PROTEIN RACD.  
GN RACD.  
OS Dictyostellium discoideum (Slime mold).  
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.  
OX NCBI\_TaxID=44689;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AX4;  
RX MEDLINE=21127961; PubMed=1122756;  
RA Rivero F., Dislich H., Glockner G., Noegel A.A.;  
RT "The Dictyostellium discoideum family of Rho-related proteins.";  
RL Nucleic Acids Res. 29:1068-1079(2001).  
RN [2]  
RP SEQUENCE OF 8-194 FROM N.A.  
RC STRAIN=AX3;  
RX MEDLINE=94124042; PubMed=8294042;  
RA Bush J.M. IV, Franek K., Cardelli J.A.;  
RT "Cloning and characterization of seven novel Dictyostellium discoideum  
rac-related genes belonging to the rho family of GTPases.";  
RL Gene 136:61-68(1993).  
CC -1- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.  
CC  
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EMBL; AF310889; AAC45121.1; -  
EMBL; L11594; AAC37390.1; -  
DR HSSP; P21181; IAM4.  
DR DictyDb; DD05066; -  
DR InterPro; IPR001806; Ras\_trnsfrmg.  
DR InterPro; IPR003578; Rho.  
PFam; PF00071; ras; 1  
DR SMART; SM00174; RHO; 1.  
KW GTP-binding.  
FT NP\_BIND 15 22 GTP (BY SIMILARITY).  
FT NP\_BIND 62 66 GTP (BY SIMILARITY).  
FT NP\_BIND 120 123 GTP (BY SIMILARITY).  
FT DOMAIN 37 45 EFFECTOR REGION (POTENTIAL).  
FT DOMAIN 9 14 POLY-VAL.  
FT DOMAIN 210 216 POLY-THR.  
FT DOMAIN 217 222 POLY-SER.  
SQ SEQUENCE 254 AA; 27530 MW; 6CA47BFDA2626BC4 CRC64;

Query Match 55.7%; Score 44; DB 1; Length 254;  
Best Local Similarity 52.9%; Pred. No. 10;  
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 SSPSSTKSSPSNVKSAS 17  
||||| | | :  
DB 198 SSPSSTKSKPSKTTT 214

RESULT 8  
NIRA\_EMENI  
ID NIRA\_EMENI STANDARD; PRT; 892 AA.  
AC P28348;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-APR-1993 (Rel. 25, Last annotation update)  
DE NITROGEN ASSIMILATION TRANSCRIPTION FACTOR NIRA.  
GN NIRA.  
OS Emericella nidulans (Aspergillus nidulans).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eurotiales; Trichocomaceae; Emericella.  
OX NCBI\_TaxID=5072;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92017856; PubMed=1922075;  
RA Burger G., Strauss J., Scazzocchio C., Lang B.F.;  
RT "nira, the pathway-specific regulatory gene of nitrate assimilation  
in Aspergillus nidulans, encodes a putative GAL4-type zinc finger  
protein and contains four introns in highly conserved regions.";  
RL Mol. Cell. Biol. 11:5746-5755(1991).  
RC  
CC -1- FUNCTION: PATHWAY-SPECIFIC REGULATORY GENE OF NITRATE  
CC ASSIMILATION; IT ACTIVATES THE TRANSCRIPTION OF THE GENES FOR  
CC NITRATE AND NITRITE REDUCTASES (NIAD AND NIIA).  
CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
CC -1- SIMILARITY: CONTAINS 1 ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR  
CC CLUSTER DOMAIN.  
CC  
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EMBL; M68900; AAA33317.1; -  
PIR; A41697; A41697.  
DR HSSP; P08657; ICID.  
DR InterPro; IPR001138; Zn2\_Cy6\_fungal.  
DR PFam; PF00172; Zn\_clus; 1.

DR SMART: SM00066; GAL4; 1.  
DR PROSITE: PS00463; ZN2\_CV6\_FUNGAL.1; 1.  
DR PROSITE: PS00463; ZN2\_CV6\_FUNGAL.2; 1.  
KW Transcription regulation; Activator; DNA-binding; Nuclear protein;  
KW Zinc: Metal-binding; Nitrate assimilation.  
FT DNA\_BIND 42 70 ZN(2)-CYS(6); FUNGAL-TYPE.  
FT DOMAIN 109 128 ASP/GLU-RICH (ACIDIC).  
FT DOMAIN 195 210 ASP/GLU-RICH (ACIDIC).  
FT DOMAIN 407 428 ASP/GLU-RICH (ACIDIC).  
FT DOMAIN 647 713 PRO-RICH.  
FT DOMAIN 842 887 PRO-RICH.  
SQ SEQUENCE 892 AA; 99448 MW; 65FD105203A53F59 CRC64;

Query Match 55.7%; Score 44; DB 1; Length 892;  
Best Local Similarity 52.9%; Pred. No. 37;  
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 SSPSSTKSSPSNVKAS 17  
Db 652 ASPSTSDSPSPSVSSQS 668  
:||||: ||:| |

RESULT 9  
ID PORA\_HORVU STANDARD; PRT; 388 AA.  
AC P13653;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE PROTOCHLOROPHYLLIDE REDUCTASE A, CHLOROPLAST PRECURSOR (EC 1.3.1.33)  
DE (PCR A) (NADPH-PROTOCHLOROPHYLLIDE OXIDOREDUCTASE A) (POR A).  
GN PORA.  
OS Hordeum vulgare (barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.  
RC STRAIN=CV. CARINA; TISSUE=leaf;  
RX MEDLINE=89364719; PubMed=271659;  
RA Schuelz R., Steinmueller K., Klaas M., Forreiter C., Rasmussen S.,  
Hillier C., Apel K.;  
RT "Nucleotide sequence of a cDNA coding for the NADPH-  
protochlorophyllide oxidoreductase (PCR) of barley (Hordeum vulgare  
L.) and its expression in Escherichia coli.";  
RL Mol. Gen. Genet. 217:355-361(1989).  
CC -1- FUNCTION: PHOTOTRANSFORMATION OF PROTOCHLOROPHYLLIDE (PCHLIDE) TO  
CHLOROPHYLLIDE (CHLIDE).  
CC -1- CATALYTIC ACTIVITY: CHLOROXYLLIDE A + NADP(+) =  
PROTOCHLOROPHYLLIDE + NADPH.  
CC -1- PATHWAY: CHLOROXYLL BIOSYNTHESIS.  
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.  
CC -1- DEVELOPMENTAL STAGE: ACTIVE ONLY TRANSIENTLY IN ETIOLATED  
SEEDLINGS AT THE BEGINNING OF ILLUMINATION.  
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
(SDR) FAMILY. POR SUBFAMILY.  
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-----  
DR EMBL: X15869; CAA33879.1; -  
DR PIR: S04783; S04783.  
DR InterPro: IPR002198; ADH\_short.  
DR Pfam: PF00106; adh\_short\_1.  
KW Photosynthesis; Chlorophyll biosynthesis; Oxidoreductase; NADP;  
Chloroplast; transit peptide; Multigene family.

FT TRANSIT 1 74 CHLOROPLAST.  
FT CHAIN 75 388 PROTOCHLOROPHYLLIDE REDUCTASE A.  
SQ SEQUENCE 388 AA; 41181 MW; EB03EF153D96C129 CRC64;

Query Match 54.4%; Score 43; DB 1; Length 388;  
Best Local Similarity 60.0%; Pred. No. 22;  
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 SSPSSTKSSPSNVKAS 15  
Db 57 TSPGSTASSPSGKKT 71  
:||||: |||:| |

RESULT 10  
ID APL\_KLULA STANDARD; PRT; 583 AA.  
AC P56095;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE AP-1-LIKE TRANSCRIPTION FACTOR.  
GN VAP1.  
OS Kluyveromyces lactis (Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
OX NCBI\_TaxID=28985;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98102743; PubMed=9439570;  
RA Billard P., Dumond H., Bolotin-Fukuhara M.;  
RT "Characterization of an AP-1-like transcription factor that mediates  
an oxidative stress response in Kluyveromyces lactis.";  
RL Mol. Gen. Genet. 257:62-70(1997).  
CC -1- FUNCTION: MEDIATES OXIDATIVE STRESS RESPONSE. INVOLVED IN BOTH THE  
OXIDATIVE AND CADMIUM RESPONSE PATHWAYS.  
CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
CC -1- SIMILARITY: TO OTHER BZIP PROTEINS.  
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-----  
DR EMBL: AF006499; AAC39320.1; -  
DR HSP: P03069; 2DGC.  
DR InterPro: IPR001871; bZIP.  
DR Pfam: PF00170; bZIP; 1.  
DR SMART: SM00338; BRLZ; 1.  
DR PROSITE: PS00036; BZIP\_BASIC; 1.  
KW Transcription regulation; DNA-binding; Activator; Nuclear protein.  
FT DNA\_BIND 38 67 BASIC MOTIF.  
FT DOMAIN 79 107 LEUCINE-ZIPPER.  
SQ SEQUENCE 583 AA; 63885 MW; A4A96B12D7F5C983 CRC64;

Query Match 54.4%; Score 43; DB 1; Length 583;  
Best Local Similarity 58.8%; Pred. No. 34;  
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 SSPSSTKSSPSNVKAS 17  
Db 214 SSISNSSSSPSNVNGLS 230  
:|:|:|:| |

RESULT 11  
ID BRC2\_HALRO STANDARD; PRT; 681 AA.  
AC BRC2\_HALRO  
DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE T-BOX CONTAINING PROTEIN 2 (AS-T2).  
 GN T2.  
 OS Halocynthia roretzi (Sea squirt).  
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;  
 OC Stolidobranchia; Pyuridae; Halocynthia.  
 OX NCBI\_TaxID=7729;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Gastrula;  
 RX MEDLINE=97115721; PubMed=8954744;  
 RA Yasuo H., Kobayashi M., Shimachi Y., Satoh N.;  
 RT "The ascidian genome contains another T-domain gene that is expressed  
 RT in differentiating muscle and the tip of the tail of the embryo.";  
 RL Dev. Biol. 180:773-779(1996).  
 CC -1- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF GENES  
 CC REQUIRED FOR MUSCLE DIFFERENTIATION. BINDS TO A PALINDROMIC  
 CC SITE (CALLED T SITE) AND ACTIVATES GENE TRANSCRIPTION WHEN BOUND  
 CC TO SUCH A SITE (BY SIMILARITY).  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: DIFFERENTIATING MUSCLE AND TAILBUD TIP.  
 CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED IN THE VEGETAL HEMISPHERE AT  
 CC UNTIL 110-CELL STAGE. EXPRESSION CONTINUES IN ENDOTHELIAL LINEAGE  
 CC IN MUSCLE LINEAGE CELLS. EXPRESSION INCREASES THROUGHOUT  
 CC GASTRULATION AND NEURULATION IN DIFFERENTIATING MUSCLE CELLS  
 CC UNTIL LATE TAILBUD STAGE. EXPRESSION ALSO DETECTED IN THE TAILBUD  
 CC TIP FROM MID-GASTRULATION TO TAIL ELONGATION.  
 CC -1- SIMILARITY: CONTAINS A T-BOX DOMAIN.  
 CC -----  
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 CC -----  
 CC EMBL: D83265; BAA19689.1; -;  
 CC HSSP: P24781; IXHR.  
 CC InterPro: IPR001699; T-box.  
 CC Pfam: PF00907; T-box; 1.  
 CC PRINTS: PR00937; TBOX.  
 CC SMART: SM00425; TBOX; 1.  
 CC PROSITE: PS01283; TBOX\_1; 1.  
 CC PROSITE: PS01284; TBOX\_2; 1.  
 CC PROSITE: PS0252; TBOX\_3; 1.  
 CC Developmental protein; Transcription regulation; DNA-binding;  
 KW Nuclear protein; Activator.  
 FT DNA\_BIND 149 323 T-BOX.  
 FT DOMAIN 127 131 POLY-GLN.  
 FT SEQUENCE 681 AA; 76430 MW; 0DD8C8C0CD54A2E5 CRC64;  
 SQ  
 Query Match 54.4%; Score 43; DB 1; Length 681;  
 Best Local Similarity 56.2%; Pred. No. 40;  
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 Oy 1 SSPSSTKSPSNVSKA 16  
 |||||: |::|::|  
 Db 478 SSPSSDSNQSNVNAS 493  
 RESULT 12  
 ID VTA2\_XENLA STANDARD; PRT; 1807 AA.  
 AC P18709; Q91895;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE VITELLOGENIN A2 PRECURSOR (VTG A2) [CONTAINS: LIPOVITELLIN I;  
 DE LIPOVITELLIN II; PHOSVITIN; PHOSVETTE I; PHOSVETTE II].  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 16-28.  
 RX MEDLINE=87259958; PubMed=3601655;  
 RA Gerber-Huber S., Nardelli D., Haefliger J.-A., Cooper D.N., Givel F.,  
 RA Germond J.-E., Engel J., Green N.M., Wahli W.;  
 RT "Precursor-product relationship between vitellogenin and the yolk  
 RT proteins as derived from the complete sequence of a Xenopus  
 RT vitellogenin gene.";  
 RL Nucleic Acids Res. 15:4737-4760(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88058863; PubMed=3680202;  
 RA Nardelli D., Het Schip F.D., Gerber-Huber S., Haefliger J.A.,  
 RA Gruber M., Ab G., Wahli W.;  
 RT "Comparison of the organization and fine structure of a chicken and a  
 RT Xenopus laevis vitellogenin gene.";  
 RL J. Biol. Chem. 262:15377-15385(1987).  
 RN [3]  
 RP SEQUENCE OF 1291-1302.  
 RX MEDLINE=90278951; PubMed=2352275;  
 RA Wallace R.A., Hoch K.L., Carnevali O.;  
 RT "Placement of small lipovitellin subunits within the vitellogenin  
 RT precursor in Xenopus laevis.";  
 RL J. Mol. Biol. 213:407-409(1990).  
 RN [4]  
 RP SEQUENCE OF 1-72 FROM N.A.  
 RX MEDLINE=85062836; PubMed=6504705;  
 RA Walker P., Germond J.-E., Brown-Luedi M., Givel F., Wahli W.;  
 RT "Sequence homologues in the region preceding the transcription  
 RT initiation site of the liver estrogen-responsive vitellogenin and  
 RT apo-VLDLII genes.";  
 RL Nucleic Acids Res. 12:8611-8626(1984).  
 CC -1- FUNCTION: PRECURSOR OF THE MAJOR EGG-YOLK PROTEINS THAT ARE  
 CC SOURCES OF NUTRIENTS DURING EARLY DEVELOPMENT OF OVIPAROUS  
 CC ORGANISMS.  
 CC -1- TISSUE SPECIFICITY: PRODUCED BY THE LIVER, SECRETED INTO THE BLOOD  
 CC AND THEN SEQUESTERED BY RECEPTOR MEDIATED ENDOCYTOSIS INTO GROWING  
 CC OOCYTES, WHERE IT IS GENERALLY CLEAVED, GIVING RISE TO THE  
 CC RESPECTIVE YOLK COMPONENTS.  
 CC -1- INDUCTION: VITELLOGENIN IS SYNTHESIZED IN THE LIVER OF OVIPAROUS  
 CC VERTEBRATES IN RESPONSE TO STEROID (ESTROGEN) INDUCTION.  
 CC -1- MISCELLANEOUS: THE SERINE-RICH PORTION OF VITELLOGENIN ENCODES  
 CC TO A LEVEL OF ABOUT 80%.  
 CC -----  
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 CC -----  
 CC EMBL: Y00354; CAA68433.1; -;  
 CC EMBL: M18061; AAA4982.1; -;  
 CC EMBL: X00205; CAA25028.1; -;  
 CC PIR: S03124; S03124.  
 CC PIR: S10625; S10625.  
 CC InterPro: IPR001747; Vitellogenin\_N.  
 CC InterPro: IPR001846; Vwd.  
 CC Pfam: PF01347; Vitellogenin\_N; 1.  
 CC Pfam: PF00094; vwd; 1.  
 CC SMART: SM00216; VWD; 1.  
 DR Storage protein; Phosphorylation; Signal; Glycoprotein.  
 KW SIGNAL 1 15  
 FT CHAIN 16 1807 VITELLOGENIN A2.  
 FT CHAIN 16 ? LIPOVITELLIN I.  
 FT CHAIN 16 ?

FT CHAIN ? 1290 PHOSVITIN (OR PHOSVETTES I + II).  
 FT CHAIN 1291 ? LIPOVITELLIN II.  
 FT DOMAIN 1126 1321 SER-RICH.  
 FT DOMAIN 1126 1163 POLY-SER.  
 FT DOMAIN 1179 1184 POLY-SER.  
 FT DOMAIN 1205 1232 POLY-SER.  
 FT DOMAIN 1263 1275 POLY-SER.  
 FT DOMAIN 1309 1321 POLY-SER.  
 FT CARBOHYD 1094 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARIANT 662 662 V -> I.  
 FT VARIANT 958 958 A -> T.  
 FT VARIANT 1572 1572 E -> K.  
 FT CONFLICT 172 72 I -> V (IN REF. 4).  
 SQ SEQUENCE 1807 AA; 201544 MW; D109B8F568147742 CRC64;

Query Match 54.4%; Score 43; DB 1; Length 1807;  
 Best Local Similarity 58.8%; Pred. NO. 1.le+02;  
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 SSPSTKSSPSNVKAS 17  
 II:II:IIII:II:II  
 DB 1145 SSSSSSSSSSSSSSS 1161

RESULT 13  
 IE18\_PRIVIF STANDARD; PRT; 1461 AA.  
 AC PII675;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE IMMEDIATE-EARLY PROTEIN IE180.  
 GN IE.  
 OS Pseudorabies virus (strain Indiana-Funkhauser / Becker) (PRV).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Varicellovirus.  
 OX NCBI\_TaxID=31523;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89315207; PubMed=2546124;  
 RA Cheung A.K.;  
 RT "DNA nucleotide sequence analysis of the immediate-early gene of pseudorabies virus.";  
 RL Nucleic Acids Res. 17:4637-4646(1989).  
 RN [2]  
 RP REVISIONS.  
 RA Cheung A.K.;  
 RL Submitted (NOV-1989) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.  
 CC -!- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.  
 CC -!- PTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF PHOSPHORYLATION.  
 CC -!- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: X15120; CAA33214.1; -.  
 DR PIR; S04713; EDBEIF.  
 DR Early protein; Transcription regulation; Trans-acting factor;  
 KW DNA-binding; Phosphorylation; Nuclear protein.  
 FT DOMAIN 390 405 POLY-SER.  
 FT DOMAIN 958 966 POLY-SER.  
 SQ SEQUENCE 1461 AA; 149833 MW; 7F31E7ABEA03B208 CRC64;

Query Match 53.8%; Score 42.5; DB 1; Length 1461;  
 Best Local Similarity 64.7%; Pred. NO. 1.le+02;  
 Matches 11; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 SSPSTKSSPSNVKAS 17  
 III:IIII:II:II:II  
 DB 853 SSPASTKSG-SSTKSSS 868

RESULT 14  
 RRA\_XENLA STANDARD; PRT; 458 AA.  
 ID RRA\_XENLA  
 AC P51126;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 20-OCT-1996 (Rel. 34, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE RETINOIC ACID RECEPTOR ALPHA (RAR-ALPHA).  
 GN RARA OR NR1B1.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92196110; PubMed=1312717;  
 RA Blumberg B., Mangelsdorf D.J., Dyck J.A., Bittner D.A., Evans R.M., de Robertis E.M.;  
 RT "Multiple retinoid-responsive receptors in a single cell: families of retinoid 'x' receptors and retinoic acid receptors in the Xenopus egg.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2321-2325(1992).  
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR RETINOIC ACID. THIS METABOLITE HAS PROFOUND EFFECTS ON VERTEBRATE DEVELOPMENT. RETINOIC ACID IS A MORPHOGEN AND IS A POWERFUL TERATOGEN. THIS RECEPTOR CONTROLS CELLS FUNCTIONS BY DIRECTLY REGULATING GENE EXPRESSION.  
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -!- DEVELOPMENTAL STAGE: IT IS SYNTHESIZED DURING OOGENESIS AND PERSISTS IN THE CLEAVING EMBRYO AT APPROXIMATELY CONSTANT LEVELS UNTIL IT IS DEGRADED JUST BEFORE GASTRULATION.  
 CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
 CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: L11445; -; NOT\_ANNOTATED\_CDS.  
 DR HSSP: P10826; 1HRA  
 DR InterPro: IPR000536; Hormone\_rec\_lig.  
 DR InterPro: IPR001723; Steroidhormone\_rcptor.  
 DR Pfam: PF00104; hormone\_rec; 1.  
 DR Pfam: PF00105; zf-C4; 1.  
 DR PRINTS; PR00047; STROIDFINGER.  
 DR PRINTS; PR00398; STRDHORMONER.  
 DR PRINTS; PR01292; RETNOICACIDR.  
 DR SMART; SM00430; HOLI; 1.  
 DR SMART; SM00399; Znf\_C4; 1.  
 DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
 KW Zinc-finger; Multigene family.  
 FT DOMAIN 1 87 MODULATING (BY SIMILARITY).  
 FT NUCLEO\_BIND 88 153 NUCLEAR RECEPTOR-TYPE.  
 FT ZN\_FING 88 108 C4-TYPE.  
 FT ZN\_FING 124 148 C4-TYPE.

Job time: 148 sec

FT DOMAIN 154 199 HINGE.  
FT DOMAIN 200 418 LIGAND-BINDING (BY SIMILARITY).  
SQ SEQUENCE 458 AA; 50573 MW; 4D80BB18678B1E17 CRC64;

Query Match 53.2%; Score 42; DB 1; Length 458;  
Best Local Similarity 90.0%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 SPSSTKSSPS 11  
      |||||  
Db 445 SPSSTHSSPS 454

RESULT 15  
YN23\_YEAST  
ID YN23\_YEAST STANDARD; PRT; 503 AA.  
AC P53832;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE HYPOTHETICAL 52.3 KDA PROTEIN IN MRPL10-ERG24 INTERGENIC REGION  
DE PRECURSOR.  
GN YNL283C OR N0583.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Messenguy F., Dubois E., Vlerendeels F., Scherens B., Pierard A.,  
RA Glansdorff N.;  
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: TO S.POMBE SPBC3D5.14C.  
CC -----  
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CC -----  
CC EMBL; Z71559; CAA96195.1; -  
CC SGD; S0005227; YNL283C.  
CC InterPro: IPR002889; WSC.  
CC Pfam; PF01822; WSC; 1.  
CC SMART; SM00321; WSC; 1.  
CC Hypothetical protein; Transmembrane; Signal.  
FT SIGNAL 1 23  
FT CHAIN 1 23  
FT CHAIN 24 503 HYPOTHETICAL PROTEIN YNL283C.  
FT TRANSMEM 61 81  
FT TRANSMEM 326 346  
FT CARBOHYD 394 394  
FT CARBOHYD 429 429  
FT CARBOHYD 475 475  
FT CARBOHYD 483 483  
FT CARBOHYD 498 498  
FT CARBOHYD 499 499  
SQ SEQUENCE 503 AA; 52292 MW; F2392A73C5CBAB50 CRC64;

Query Match 53.2%; Score 42; DB 1; Length 503;  
Best Local Similarity 52.9%; Pred. No. 41;  
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 1 SSPSSTKSSPSNVKSAS 17  
      ||:|||||  
Db 203 SSTTSTSSSPSTTSST 219

Search completed: January 29, 2002, 11:16:19

us-09-763-397a-22.rsp

Mon Feb 4 15:23:44 2002

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 11:12:20 ; Search time 62.77 Seconds  
(without alignments)  
39.615 Million cell updates/sec

Title: US-09-763-397A-22

Perfect score: 79  
Sequence: 1 SSPSSTKSSPSNVKSAS 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL\_17:\*
- 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phase:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68.5	86.7	171	5 Q26002	Q26002 plasmodium
2	68.5	86.7	171	5 Q26003	Q26003 plasmodium
3	68.5	86.7	782	5 Q25730	Q25730 plasmodium
4	68.5	86.7	782	5 Q25675	Q25675 plasmodium
5	68.5	86.7	782	5 Q26007	Q26007 plasmodium
6	68.5	86.7	782	5 Q9U431	Q9U431 plasmodium
7	68.5	86.7	782	5 Q9U430	Q9U430 plasmodium
8	68.5	86.7	782	5 Q9U429	Q9U429 plasmodium
9	68.5	86.7	782	5 Q9U414	Q9U414 plasmodium
10	65.5	82.9	782	5 Q26104	Q26104 plasmodium
11	62.5	79.1	292	5 Q25762	Q25762 plasmodium
12	50	63.3	2559	5 Q9V7X3	Q9V7X3 drosophila
13	49	62.0	493	11 Q9JKN6	Q9JKN6 mus musculus
14	48	60.8	328	10 O81138	O81138 arabidopsis
15	47	59.5	98	5 Q9NPH0	Q9NPH0 plasmodium
16	47	59.5	215	13 Q98TQ9	Q98TQ9 gallus gall
17	47	59.5	497	2 Q9PAB6	Q9PAB6 xylella fas
18	47	59.5	795	5 Q9YIJ5	Q9YIJ5 dictyosteli
19	46	58.2	243	11 Q9QY63	Q9QY63 mus musculus

20	46	58.2	244	4 Q9Y4S1	Q9Y4S1 homo sapien
21	46	58.2	312	10 Q9LHF0	Q9LHF0 arabidopsis
22	46	58.2	1514	4 Q9P2F8	Q9P2F8 homo sapien
23	45	57.0	211	10 Q9LPE8	Q9LPE8 arabidopsis
24	45	57.0	349	3 Q74947	Q74947 schizosacch
25	45	57.0	383	5 Q9GWA1	Q9GWA1 leishmania
26	45	57.0	590	11 O88337	O88337 rattus norv
27	45	57.0	625	11 Q9ROU2	Q9ROU2 mus musculu
28	45	57.0	626	11 O88295	O88295 mus musculu
29	45	57.0	626	11 O88529	O88529 mesocricetu
30	45	57.0	626	11 O88810	O88810 rattus norv
31	45	57.0	632	11 Q9WTL8	Q9WTL8 mus musculu
32	45	57.0	633	13 Q918T7	Q918T7 gallus gall
33	45	57.0	766	12 Q9DMF7	Q9DMF7 rat cytomeg
34	45	57.0	2406	5 Q9VXM5	Q9VXM5 drosophila
35	45	57.0	2559	5 O44113	O44113 drosophila
36	45	57.0	2559	5 O44381	O44381 drosophila
37	44	55.7	103	4 O60372	O60372 homo sapien
38	44	55.7	163	4 Q9NPN4	Q9NPN4 homo sapien
39	44	55.7	214	10 O49780	O49780 arabidopsis
40	44	55.7	229	10 O81864	O81864 arabidopsis
41	44	55.7	254	4 Q9UIX6	Q9UIX6 homo sapien
42	44	55.7	267	10 Q9W9U2	Q9W9U2 arabidopsis
43	44	55.7	311	4 Q9NWX1	Q9NWX1 homo sapien
44	44	55.7	337	5 O16139	O16139 lytechinus
45	44	55.7	398	3 Q9HED1	Q9HED1 neurospora

ALIGNMENTS

RESULT 1  
Q26002 PRELIMINARY: PRT; 171 AA.  
AC Q26002;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE RHOPTRY PROTEIN (FRAGMENT).  
GN RAP-1.  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SIERRA LEONE;  
RX MEDLINE=92244303; PubMed=1574089;  
RA Howard R.F.;  
RT "The sequence of the p82 rhoptry protein is highly conserved between two Plasmodium falciparum isolates";  
RL Mol. Biochem. Parasitol. 51:327-330(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SIERRA LEONE;  
RX MEDLINE=93293317; PubMed=7685740;  
RA Howard R.F., Jensen J.B., Franklin H.L.;  
RT "Reactivity profile of human anti-82-kilodalton rhoptry protein antibodies generated during natural infection with Plasmodium falciparum";  
RL Infect. Immun. 61:2960-2965(1993).  
DR EMBL: L10322; AAB59202.1; -;  
FT NON\_TER 1  
FT NON\_TER 171  
SQ SEQUENCE 171 AA; 18510 MW; 8BF570908D3DB844 CRC64;

Query Match 86.7%; Score 68.5; DB 5; Length 171;  
Best Local Similarity 94.4%; Pred. No. 0.0015;  
Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SSPSSTK-SSPSNVKSAS 17  
||||| |||||||  
DB 22 SSPSSTKSSPSNVKSAS 39

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RESULT 2
Q26003
ID Q26003 PRELIMINARY; PRT; 171 AA.
AC Q26003;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE RHOPTRY PROTEIN (FRAGMENT).
GN RAP-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TANZANIA I/CDC;
MEDLINE=92244303; PubMed=1574089;
RA Howard R.F.;
RT "The sequence of the p82 rhoptry protein is highly conserved between
RT two Plasmodium falciparum isolates.";
RL Mol. Biochem. Parasitol. 51:327-330(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-TANZANIA I/CDC;
MEDLINE=93293317; PubMed=7685740;
RA Howard R.F.; Jensen J.B.; Franklin H.L.;
RT "Reactivity profile of human anti-82-kilodalton rhoptry protein
RT antibodies generated during natural infection with Plasmodium
RT falciparum.";
RL Infect. Immun. 61:2960-2965(1993).
DR EMBL; L10323; AAA29742.1; -.
FT NON_TER 1
FT SEQUENCE 171 AA; 18531 MW; 192CBACFC68970CB8 CRC64;
SQ SEQUENCE 171 AA; 18531 MW; 192CBACFC68970CB8 CRC64;

Query Match 86.7%; Score 68.5; DB 5; Length 171;
Best Local Similarity 94.4%; Pred. No. 0.0015;
Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SSPSTK-SSPSNVKSAS 17
||||| |||||||
DB 22 SSPSTKSSPSNVKSAS 39

RESULT 3
Q25730
ID Q25730 PRELIMINARY; PRT; 782 AA.
AC Q25730;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE RHOPTRY ASSOCIATED PROTEIN-1.
GN RAP-1.
OS Plasmodium falciparum (isolate FC27 / Papua New Guinea).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5837;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FC27;
RA Shi Y.; Lai A.A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U20985; AAA63681.1; -.
SQ SEQUENCE 782 AA; 90023 MW; F69E26A2A564C8EA CRC64;

Query Match 86.7%; Score 68.5; DB 5; Length 782;
Best Local Similarity 94.4%; Pred. No. 0.0059;
Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SSPSTK-SSPSNVKSAS 17
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DB 145 SSPSTKSSPSNVKSAS 162

RESULT 4
Q25875
ID Q25875 PRELIMINARY; PRT; 782 AA.
AC Q25875;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE PR86 RHOPTRY PRECURSOR PROTEIN.
GN PR86.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HONDURAS I CDC;
MEDLINE=90348711; PubMed=2200961;
RA Ridley R.G.; Takacs B.; Lahm H.W.; Delves C.J.; Goman M.; Certa V.;
RA Matile H.; Woollett G.R.; Scaife J.G.;
RT "Characterisation and sequence of a protective rhoptry antigen from
RT Plasmodium falciparum.";
RL Mol. Biochem. Parasitol. 41:125-134(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HONDURAS I CDC;
MEDLINE=92244303; PubMed=1574089;
RA Howard R.F.;
RT "The sequence of the p82 rhoptry protein is highly conserved between
RT two Plasmodium falciparum isolates.";
RL Mol. Biochem. Parasitol. 51:327-330(1992).
DR EMBL; M80807; AAA29717.1; -.
SQ SEQUENCE 782 AA; 90096 MW; D1AD099862528D42 CRC64;

Query Match 86.7%; Score 68.5; DB 5; Length 782;
Best Local Similarity 94.4%; Pred. No. 0.0039;
Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SSPSTK-SSPSNVKSAS 17
||||| |||||||
DB 145 SSPSTKSSPSNVKSAS 162

RESULT 5
Q26007
ID Q26007 PRELIMINARY; PRT; 782 AA.
AC Q26007;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE RHOPTRY ASSOCIATED PROTEIN 1 (ROPI) PRECURSOR (FRAGMENT).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=90348711; PubMed=2200961;
RA Ridley R.G.; Takacs B.; Lahm H.W.; Delves C.J.; Goman M.; Certa V.;
RA Matile H.; Woollett G.R.; Scaife J.G.;
RT "Characterisation and sequence of a protective rhoptry antigen from
RT Plasmodium falciparum.";
RL Mol. Biochem. Parasitol. 41:125-134(1990).
DR EMBL; M32853; AAA29753.1; -.
SQ SEQUENCE 782 AA; 90080 MW; 2F2E240D40A4C902 CRC64;

Query Match 86.7%; Score 68.5; DB 5; Length 782;
Best Local Similarity 94.4%; Pred. No. 0.0059;
Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SSPSTK-SSPSNVKSAS 17
||||| |||||||
DB 145 SSPSTKSSPSNVKSAS 162

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Best Local Similarity 94.4%; Pred. No. 0.0059;  
Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SSPSSTK-SSPSNVKSAS 17  
Db 145 SSPSSTKSSPSNVKSAS 162

RESULT 6

Q9U431 ID Q9U431 PRELIMINARY; PRT; 782 AA.  
AC Q9U431;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE RHOPTRY-ASSOCIATED PROTEIN 1 (FRAGMENT).  
GN RAP1.  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Saul A.;  
RT "Efficacy of vaccines containing Rhoptyr-Associated Proteins RAP1 and  
RAP2 of Plasmodium falciparum in Saimiri boliviensis monkeys.";  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF205282; AAF23403.1; -.  
FT NON\_TER 782  
SQ SEQUENCE 782 AA; 90066 MW; B344948D5806F7DC CRC64;

Query Match 86.7%; Score 68.5; DB 5; Length 782;  
Best Local Similarity 94.4%; Pred. No. 0.0059;  
Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SSPSSTK-SSPSNVKSAS 17  
Db 145 SSPSSTKSSPSNVKSAS 162

RESULT 7

Q9U430 ID Q9U430 PRELIMINARY; PRT; 782 AA.  
AC Q9U430;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE RHOPTRY-ASSOCIATED PROTEIN 1 (FRAGMENT).  
GN RAP1.  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FUP;  
RA Saul A.;  
RT "Efficacy of vaccines containing Rhoptyr-Associated Proteins RAP1 and  
RAP2 of Plasmodium falciparum in Saimiri boliviensis monkeys.";  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF205283; AAF23404.1; -.  
FT NON\_TER 782  
SQ SEQUENCE 782 AA; 90131 MW; A0FCB64529C34E59 CRC64;

Query Match 86.7%; Score 68.5; DB 5; Length 782;  
Best Local Similarity 94.4%; Pred. No. 0.0059;  
Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SSPSSTK-SSPSNVKSAS 17  
Db 145 SSPSSTKSSPSNVKSAS 162

RESULT 8

Q9U429 ID Q9U429 PRELIMINARY; PRT; 782 AA.  
AC Q9U429;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE RHOPTRY-ASSOCIATED PROTEIN 1.  
GN RAP1.  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVO;  
RA Saul A.;  
RT "Efficacy of vaccines containing Rhoptyr-Associated Proteins RAP1 and  
RAP2 of Plasmodium falciparum in Saimiri boliviensis monkeys.";  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF205284; AAF23405.1; -.  
SQ SEQUENCE 782 AA; 90041 MW; 27F2EA9BC930434E CRC64;

Query Match 86.7%; Score 68.5; DB 5; Length 782;  
Best Local Similarity 94.4%; Pred. No. 0.0059;  
Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SSPSSTK-SSPSNVKSAS 17  
Db 145 SSPSSTKSSPSNVKSAS 162

RESULT 9

Q9U414 ID Q9U414 PRELIMINARY; PRT; 782 AA.  
AC Q9U414;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE RHOPTRY ASSOCIATED PROTEIN-1.  
GN RAP-1.  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FCCL7HN;  
RA Li X.R., Luo S.H., Yu X.B., Shan Z.X., Ma C.L.;  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF206631; AAF15365.1; -.  
SQ SEQUENCE 782 AA; 90082 MW; 8E1F4CF2883903FD CRC64;

Query Match 86.7%; Score 68.5; DB 5; Length 782;  
Best Local Similarity 94.4%; Pred. No. 0.0059;  
Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SSPSSTK-SSPSNVKSAS 17  
Db 145 SSPSSTKSSPSNVKSAS 162

RESULT 10

Q26104 ID Q26104 PRELIMINARY; PRT; 782 AA.  
AC Q26104;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE RHOPTRY ASSOCIATED PROTEIN 1.  
GN RAP-1.  
OS Plasmodium reichenowi.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Mon Feb 4 15:23:44 2002

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OX NCBI_TaxID=5854;
RN [1]
RP SEQUENCE FROM N.A.
RA Shi Y., Lal A.A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U20986; AAA63682.1; -
SQ SEQUENCE 782 AA; 90160 MW; DE6D1BE2FAC308A9 CRC64;

Query Match      82.9%; Score 65.5; DB 5; Length 782;
Best Local Similarity 88.9%; Pred. No. 0.018;
Matches 16; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

OY 1 SSPSSTK-SSPSNVKAS 17
Db 145 SSPSSTKSSPSNVKTAS 162
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RESULT 11
Q25762 PRELIMINARY; PRT; 292 AA.
AC Q25762;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE STRAIN INDD RHOPTRY-ASSOCIATED PROTEIN 1 (RAP-1) (FRAGMENT).
GN RAP-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-INDD (INDIAN ISOLATE D);
RX MEDLINE=92244303; PubMed=1574089;
RA Howard R.F.;
RT "The sequence of the p82 rhoptry protein is highly conserved between
RT two Plasmodium falciparum isolates."
RL Mol. Biochem. Parasitol. 51:327-330(1992).
[2]
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-INDD (INDIAN ISOLATE D);
RX MEDLINE=96379224; PubMed=8784775;
RA Howard R.F., Peterson C.;
RT "Limited RAP-1 sequence diversity in field isolates of Plasmodium
RT falciparum."
RL Mol. Biochem. Parasitol. 77:95-98(1996).
DR EMBL; U41074; AAC47090.1; -
DR NON_TER 292 1
FT NON_TER 292 1
SQ SEQUENCE 292 AA; 32345 MW; A35C979C3FEC3019 CRC64;

Query Match      79.1%; Score 62.5; DB 5; Length 292;
Best Local Similarity 88.9%; Pred. No. 0.022;
Matches 16; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 SSPSSTK-SSPSNVKAS 17
Db 139 SSPSITKSSSPSNVKSAS 156
||||||| ||||||| |||

RESULT 12
Q9V7X3 PRELIMINARY; PRT; 2559 AA.
AC Q9V7X3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE RHOGF2 PROTEIN.
GN RHOGF2 OR CG9635.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

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OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt J., Nelson C.R., Miklos G.L.G.,
RA April J.F., Adayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies K.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Moberg C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhou X.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003804; AAF57915.1; -
DR HSP; Q12923; 3PDZ.
DR FlyBase; FBgn023172; RhogEF2.
DR InterPro; IPR001525; C5_DNA_meth.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; RhogEF.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00595; PDZ; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhogEF; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00228; PDZ; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhogEF; 1.
DR PROSITE; PS00094; C5_MTASE_1; UNKNOWN_1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS0106; PDZ; 1.
SQ SEQUENCE 2559 AA; 280805 MW; 07725DE04982605C CRC64;

Query Match      63.3%; Score 50; DB 5; Length 2559;
Best Local Similarity 76.9%; Pred. No. 14;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 PSSSTKSSPSNVKS 15
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Db 645 PSSTDSPSNAKS 657

## RESULT 13

Q9JKN6 PRELIMINARY; PRT; 493 AA.  
AC Q9JKN6; 493 AA.  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE VENTRAL NEURON-SPECIFIC PROTEIN 1 NOVAL (FRAGMENT).  
GN NOVAL.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CBA/J; TISSUE=BRAIN;  
RA Ward-Bailey P.F., Johnson K.R.;  
RT "Neuromuscular ataxia: a new spontaneous mutation in the mouse."  
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF232828; AAF35907.1;  
DR MGD; MGI:104297; Noval.  
DR InterPro; IPR000958; KH.  
DR Pfam; PF00013; KH-domain; 3.  
DR SMART; SM00322; KH; 3.  
FT NON\_TER 1  
SQ SEQUENCE 493 AA; 50302 MW; 7D09E8A55B0A7817 CRC64;

Query Match 62.0%; Score 49; DB 11; Length 493;

Best Local Similarity 58.8%; Pred. No. 4.8;

Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SSPSTKSSPSNVKAS 17

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Db 139 SSPTTKSSPSDPMTTS 155

## RESULT 14

O81138 PRELIMINARY; PRT; 328 AA.  
AC O81138;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE AP2 DOMAIN FAMILY TRANSCRIPTION FACTOR HOMOLOG.  
GN AB14 OR AT2G40220.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. COLUMBIA;  
RX MEDLINE=98299844; Pubmed=9634591;  
RA Finkelstein R.R., Wang M.L., Lynch T.J., Rao S., Goodman H.M.;  
RT "The Arabidopsis abscisic acid response locus AB14 encodes an APETALA  
RT 2 domain protein."  
RL Plant Cell 10:1043-1054(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99225673; Pubmed=10207155;  
RA Wang M.L., Belmonte S., Kim U., Dolan M., Morris J.W., Goodman H.M.;  
RT "A cluster of ABA-regulated genes on Arabidopsis thaliana BAC  
RT T07M07."  
RL Genome Res. 9:325-333(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. COLUMBIA;  
RX MEDLINE=20083487; Pubmed=10617197;

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,  
RA Buell C.R., Ketchum K.A., Lee J.-J., Ronning C.M., Koo H., Moffat K.S.,  
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,  
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,  
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,  
RA Salzberg S.L., Fraser C.M., Venter J.C.;  
RT "Sequence and analysis of chromosome II of Arabidopsis thaliana."  
RL Nature 402:761-768(1999).  
DR EMBL: AF040959; AAC39489.1;  
DR EMBL: AF085279; AAD25937.1;  
DR EMBL: AC018721; AAF18736.1;  
DR HSP; O80337; 2GCC.  
DR TRANSFAC; T02642;  
DR InterPro; IPR001471; AP2-domain.  
DR Pfam; PF00847; AP2-domain; 1.  
DR PRINTS; PR00367; ETHRSPELEMNT.  
DR ProDom; PD001423; AP2-domain; 1.  
DR SMART; SM00380; AP2; 1.  
SQ SEQUENCE 328 AA; 35671 MW; B6B710475E34D08F CRC64;

Query Match 60.8%; Score 48; DB 10; Length 328;

Best Local Similarity 64.7%; Pred. No. 4.8;

Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SSPSTKSSPSNVKAS 17

|||||:|||||:|

Db 113 SSPSSVSSSSSVSAAS 129

## RESULT 15

Q9NFH0 PRELIMINARY; PRT; 98 AA.  
AC Q9NFH0;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE HYPOTHETICAL 9.6 KDA PROTEIN (FRAGMENT).  
OS Plasmodium falciparum (isolate 3D7).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=36329;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=3D7;  
RA Spielmann T., Beck H.;  
RT "Analysis of stage specific transcription in Plasmodium falciparum  
RT reveals a set of genes exclusively transcribed in ring stage  
RT parasites."  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ290927; CAB92936.1;  
KW Hypothetical protein.  
FT NON\_TER 1  
FT NON\_TER 98  
SQ SEQUENCE 98 AA; 9590 MW; BC1857EB0D303042 CRC64;

Query Match 59.5%; Score 47; DB 5; Length 98;

Best Local Similarity 62.5%; Pred. No. 2.4;

Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 SSPSTKSSPSNVKAS 17

|||||:|||||:|

Db 14 SPSSSSSSPSSSSSS 29

Search completed: January 29, 2002, 11:15:52

Job time: 212 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 10:59:18 ; Search time 66.28 Seconds  
(without alignments)  
18.999 Million cell updates/sec

Title: US-09-763-397A-23

Perfect score: 84

Sequence: 1 LATRLMKFKAEIRDFF 17

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	100.0	17	AAV70299	Plasmodium falcipa
2	84	100.0	350	AAV70278	Recombinant vaccin
3	84	100.0	782	AAV70299	Polypeptide antige
4	45	53.6	190	AAV70299	S. epidermidis ope
5	45	53.6	1572	AAV70299	S. epidermidis ope
6	43	51.2	86	AAV70299	Gene 36 human secr
7	43	51.2	86	AAV70299	Human secreted pro
8	43	51.2	98	AAV70299	Human prostate can
9	43	51.2	297	AAV70299	Arabidopsis thalia
10	43	51.2	335	AAV70299	Arabidopsis thalia
11	43	51.2	353	AAV70299	Arabidopsis thalia

12	42	50.0	186	21	AAG04103	Arabidopsis thalia
13	42	50.0	190	21	AAG04102	Arabidopsis thalia
14	42	50.0	203	21	AAG04101	Arabidopsis thalia
15	41	48.8	300	21	AAG07741	Arabidopsis thalia
16	41	48.8	300	21	AAG38362	Arabidopsis thalia
17	41	48.8	302	21	AAG07740	Arabidopsis thalia
18	41	48.8	302	21	AAG38361	Arabidopsis thalia
19	41	48.8	319	21	AAG07739	Arabidopsis thalia
20	41	48.8	319	21	AAG38360	Arabidopsis thalia
21	41	48.8	2325	17	AAW05590	Maize acetyl CoA c
22	41	48.8	2325	19	AAW56736	Maize ACCase enzym
23	41	48.8	2325	21	AAW44687	Maize acetyl CoA c
24	40	47.6	333	21	AAG05123	Arabidopsis thalia
25	40	47.6	333	21	AAG50040	Arabidopsis thalia
26	40	47.6	338	21	AAG05122	Arabidopsis thalia
27	40	47.6	338	21	AAG50039	Arabidopsis thalia
28	40	47.6	356	21	AAG05121	Arabidopsis thalia
29	40	47.6	356	21	AAG50038	Arabidopsis thalia
30	40	47.6	534	21	AAV77232	Maize cytochrome p
31	40	47.6	534	21	AAV44726	Maize cytochrome p
32	39	46.4	247	20	AAV06357	Chaetomium brasill
33	39	46.4	247	21	AAV14870	Chaetomium brasill
34	39	46.4	247	21	AAV84335	Amino acid sequenc
35	39	46.4	375	21	AAG23212	Arabidopsis thalia
36	39	46.4	423	21	AAG23211	Arabidopsis thalia
37	39	46.4	485	21	AAG23210	Arabidopsis thalia
38	39	46.4	1147	14	AAV41199	CAI antigen. Heli
39	39	46.4	1338	19	AAV80600	Helicobacter pylor
40	38.5	45.8	133	21	AAV33094	Pinus radiata tran
41	38	45.2	281	19	AAV72190	HSV-2 strain SB5 C
42	38	45.2	354	19	AAV72122	HSV-2 strain SB5 C
43	38	45.2	354	19	AAV72045	HSV-2 strain SB5 C
44	38	45.2	475	21	AAG50384	Arabidopsis thalia
45	38	45.2	539	21	AAG50383	Arabidopsis thalia

#### ALIGNMENTS

RESULT 1  
AAV70299  
ID AAV70299 standard; peptide; 17 AA.  
XX  
AC AAV70299;  
XX  
DT 06-JUN-2000 (first entry)  
XX  
DE Plasmodium falciparum RAP-1 antigenic epitope, P605.  
XX  
KW Recombinant protein; CDC/NIAIDVAC-1; multivalent; malaria; vaccine;  
KW T-cell epitope; tetanus toxoid; antigenic epitope; treatment;  
KW circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2;  
KW liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2;  
KW apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175;  
KW EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen;  
KW Pf27; antiparasitic; prevention; anti-CDC/NIAIDVAC-1 antibody.  
XX  
OS Plasmodium falciparum.  
XX  
PN WO200011179-A1.  
XX  
PD 02-MAR-2000.  
XX  
PF 19-AUG-1999; 99WO-US18869.  
XX  
PR 21-AUG-1998; 98US-0097703.  
XX  
PA (NAIM-) NAT INST IMMUNOLOGY.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
PI Lal AA, Shi YP, Hasnain SE;  
XX WPI; 2000-237654/20.  
DR

Mon Feb 4 15:23:44 2002

```

XX PA (NAIM-) NAT INST IMMUNOLOGY.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Lal AA, Shi YP, Hasnain SE;
XX DR WPI: 2000-237654/20.
XX DR N-PSDB; RAZ51336.
XX
XX Novel recombinant protein as vaccine for treating malarial infection
XX PT comprises antigenic peptides obtained from different stages of
XX PT plasmodium falciparum life cycle
XX
XX Claim 3; Page 43-44; 52pp; English.
XX
XX The present sequence is that of recombinant protein CDC/NIIMALVAC-1,
XX CC which is a multivalent, multistage malarial vaccine. The recombinant
XX CC protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope
XX CC from tetanus toxoid and 21 antigenic epitopes from circumsporozoite
XX CC protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage
XX CC antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical
XX CC membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175),
XX CC rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pf27.
XX CC These epitopes were obtained at different stages of the life cycle of
XX CC Plasmodium falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic
XX CC activity and can be used for treatment and prevention of malarial
XX CC infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting
XX CC P. falciparum in biological samples.
XX
XX Sequence 17 AA:
XX
XX Query Match 100.0%; Score 84; DB 21; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-07;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LATRLMKFKAEIRDF 17
XX Db 1 latrlmkfkaeirdff 17
XX
XX RESULT 2
XX ID AAY70278 standard; Protein; 350 AA.
XX AC AAY70278;
XX
XX DT 06-JUN-2000 (first entry)
XX DE Recombinant vaccine CDC/NIIMALVAC-1.
XX
XX KW Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine;
XX KW T-cell epitope; tetanus toxoid; antigenic epitope; treatment;
XX KW circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2;
XX KW liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2;
XX KW apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175;
XX KW EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen;
XX KW Pf27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody;
XX KW honey bee.
XX
XX OS Chimeric - Apis sp.
XX OS Chimeric - Clostridium tetani.
XX OS Chimeric - Plasmodium falciparum.
XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..22 Melittin signal peptide
XX FT /label= "Melittin signal peptide"
XX FT /note= "Derived from Honey bee"
XX
XX FT Protein 23..350 Mature CDC/NIIMALVAC-1
XX FT /label=
XX FT /note= "Recombinant multivalent malarial vaccine"
XX
XX WO200011179-A1.
XX
XX PD 02-MAR-2000.
XX
XX PF 19-AUG-1999; 99WO-US18869.
XX
XX PR 21-AUG-1998; 98US-0097703.

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XX PA (NAIM-) NAT INST IMMUNOLOGY.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Lal AA, Shi YP, Hasnain SE;
XX DR WPI: 2000-237654/20.
XX DR N-PSDB; RAZ51336.
XX
XX Novel recombinant protein as vaccine for treating malarial infection
XX PT comprises antigenic peptides obtained from different stages of
XX PT plasmodium falciparum life cycle
XX
XX Claim 3; Page 43-44; 52pp; English.
XX
XX The present sequence is that of recombinant protein CDC/NIIMALVAC-1,
XX CC which is a multivalent, multistage malarial vaccine. The recombinant
XX CC protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope
XX CC from tetanus toxoid and 21 antigenic epitopes from circumsporozoite
XX CC protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage
XX CC antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical
XX CC membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175),
XX CC rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pf27.
XX CC These epitopes were obtained at different stages of the life cycle of
XX CC Plasmodium falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic
XX CC activity and can be used for treatment and prevention of malarial
XX CC infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting
XX CC P. falciparum in biological samples.
XX
XX Sequence 350 AA:
XX
XX Query Match 100.0%; Score 84; DB 21; Length 350;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-06;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LATRLMKFKAEIRDF 17
XX Db 317 latrlmkfkaeirdff 333
XX
XX RESULT 3
XX ID AAR06991 standard; protein; 782 AA.
XX AC AAR06991;
XX
XX DT 16-JAN-1991 (first entry)
XX DE Polypeptide antigenic to rhostry organelles of Plasmodium.
XX
XX KW Malaria; vaccine; rhostry organelles..
XX
XX OS Plasmodium falciparum.
XX
XX PN EP388738-A.
XX
XX PD 26-SEP-1990.
XX
XX PF 09-MAR-1990; 90EP-0104561.
XX
XX PR 22-AUG-1989; 89GB-0019064.
XX PR 14-MAR-1989; 89GB-0005857.
XX
XX FA (HOFF ) HOFFMANN-LA ROCHE AG.
XX
XX PI Ridley RG, Scaife JG;
XX
XX DR WPI: 1990-291721/39.
XX DR N-PSDB; AAQ06000.
XX
XX PT Antigenic polypeptide and DNA encoding it - having a determinant
XX PT cross reactive with those on the rhostry organelles of the

```



PT merozoite form of the malaria parasite P falciparum.

XX PS Claim 1: Fig 2a-b; 29pp; English.

XX CC Gene product may be isolated from a transformed E.coli (Y1088)

XX CC expression system using plasmid pMC9, and may then be used for

XX CC immunisation against malaria. The product may also be used

XX CC diagnostically to detect Abs directed against the parasite.

XX SQ Sequence 782 AA;

Query Match 100.0%; Score 84; DB 11; Length 782;

Best Local Similarity 100.0%; Pred. NO. 7.5e-06;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LATRLMKKFKAEIRDFF 17

|||||

Db 736 latrimkkfkaeirdff 752

RESULT 4

AAG82568

ID AAG82568 standard; Protein; 190 AA.

XX AC AAG82568;

DT 03-SEP-2001 (first entry)

XX DE S. epidermidis open reading frame protein sequence SEQ ID NO:2230.

XX KW Staphylococcus epidermidis SRI strain; infection; diagnosis;

XX KW vaccination; endocarditis.

XX OS Staphylococcus epidermidis.

XX PN WO200134809-A2.

XX PD 17-MAY-2001.

XX PF 09-NOV-2000; 2000WO-US30782.

XX PR 09-NOV-1999; 99US-0164258.

XX PA (GLAX ) GLAXO GROUP LTD.

XX PI Kimmerly WJ;

XX DR WPI; 2001-316495/33.

XX DR N-PSDB; AAG82568.

XX PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,

XX PT useful for vaccinating against infections, e.g. endocarditis -

XX PS Claim 18; Page 597; 2188pp; English.

XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides

XX CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.

XX CC (I) and (II) can have antibacterial activity and therefore can be used

XX CC in vaccination. The nucleic acids (I) may be used to produce the

XX CC S. epidermidis polypeptides (II) via the production of vectors

XX CC containing them which are used to produce hosts cells which express the

XX CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be

XX CC used to vaccinate subjects and to raise antibodies against the bacteria.

XX CC The polypeptides may also be used to assay for other inhibitors of their

XX CC activity and therefore identify compounds that may be used for the

XX CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to

XX CC AAH5090 represent specifically claimed S. epidermidis genomic DNA

XX CC polynucleotide sequences from the present invention. AAH55091 to

XX CC AAH55098 represent oligonucleotide sequences and primers which are used

XX CC N.B. The present invention specifically claims all the polynucleotide

XX CC sequences given in the sequence listing of the present specification,

CC however the sequence listing only goes up to SEQ ID NO:4454 so even

CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,

CC no sequences are present for SEQ ID NO:4455 to 4464.

XX SQ Sequence 190 AA;

Query Match 53.6%; Score 45; DB 22; Length 190;

Best Local Similarity 52.9%; Pred. NO. 5.3;

Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LATRLMKKFKAEIRDFF 17

|||::|||

Db 120 lmtamikkknkgikdff 136

RESULT 5

AAG82906

ID AAG82906 standard; Protein; 1572 AA.

XX AC AAG82906;

DT 03-SEP-2001 (first entry)

XX DE S. epidermidis open reading frame protein sequence SEQ ID NO:2906.

XX KW Staphylococcus epidermidis SRI strain; infection; diagnosis;

XX KW vaccination; endocarditis.

XX OS Staphylococcus epidermidis.

XX PN WO200134809-A2.

XX PD 17-MAY-2001.

XX PF 09-NOV-2000; 2000WO-US30782.

XX PR 09-NOV-1999; 99US-0164258.

XX PA (GLAX ) GLAXO GROUP LTD.

XX PI Kimmerly WJ;

XX DR WPI; 2001-316495/33.

XX DR N-PSDB; AAH53756.

XX PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,

XX PT useful for vaccinating against infections, e.g. endocarditis -

XX PS Claim 18; Page 759; 2188pp; English.

XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides

XX CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.

XX CC (I) and (II) can have antibacterial activity and therefore can be used

XX CC in vaccination. The nucleic acids (I) may be used to produce the

XX CC S. epidermidis polypeptides (II) via the production of vectors

XX CC containing them which are used to produce hosts cells which express the

XX CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be

XX CC used to vaccinate subjects and to raise antibodies against the bacteria.

XX CC The polypeptides may also be used to assay for other inhibitors of their

XX CC activity and therefore identify compounds that may be used for the

XX CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to

XX CC AAH5090 represent specifically claimed S. epidermidis genomic DNA

XX CC polynucleotide sequences from the present invention. AAH55091 to

XX CC AAH55098 represent oligonucleotide sequences and primers which are used

XX CC N.B. The present invention specifically claims all the polynucleotide

XX CC sequences given in the sequence listing of the present specification,

XX CC however the sequence listing only goes up to SEQ ID NO:4454 so even

XX CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,

XX CC no sequences are present for SEQ ID NO:4455 to 4464.

XX SQ Sequence 1572 AA;

Query Match	53.6%	Score 45;	DB 22;	Length 1572;
Best Local Similarity	52.9%	Pred. No. 48;		
Matches	9;	Conservative	3;	Mismatches
			5;	Indels

Qy 1 LATRLMKKFAEIRDF 17  
| | : | | | : | |  
pb 1161 lmtamikkllknqikdfff 1177

RESULT 6  
AAB44822  
ID AAB44822 standard: Protein: 86 AA:

AC AAB44822:

12-FEB-2001 (first entry)

XX 26 human secreted protein homologous amino acid sequence #121.

XX Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;  
 KW antirheumatic; antiproliferative; cytostatic; cardiac; vasotropic;  
 KW cerebroprotective; neotropic; neuroprotective; antibacterial; virucide;  
 KW fungicide; ophthalmological; gene therapy; autoimmune disease; infection;  
 KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;  
 KW cerebrovascular disorder; nervous system disorder; ocular disorder;  
 KW eye disease; skin aging; food additive; preservative.

OS Homo sapiens.

AA PN WO200058336-A1.

05-OCT-2000;

23-MAR-2000:

XX  
PR 26-MAR-1999; 99US-0126597.

PR 07-JAN-2006, 20060301, 01, 00, XX

PA	(HUMA-)	HUMAN GENOME	SCI. INCT.
XX			
PI	Rosen CA.	Ruben SM.	Komatsoulis G;

WPT: 2000-602355/57.

xx Nucleic/acid encoding human secreted proteins, used to treat, prevent,  
pt ameliorate or diagnose medical conditions such as cancer, and  
pt autoimmune diseases -  
nm

XX  
ps disclosure: page 380-381: 391pp: English.

The polynucleotide sequences given in AAC79799 to AAC79848 encode the human secreted proteins given in AAB44762 to AAB44811. ABA44812 to AAB44829 represent human secreted polypeptide sequences and proteins homologous to them, which are used in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities are: immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide; fungicide; and ophthalmological. The polynucleotides and polypeptides can be used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases, hyperproliferative disorders, cardiovascular disorders, cerebrovascular disorders, angiogenests, nervous system disorders, infections caused by bacteria, viruses and fungi and ocular disorders. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of neonatal tissues to regenerate tissues and in chemotaxis. The

3

CC polypeptides can also be used as a food additive or preservative to  
CC increase or decrease storage capabilities. AAC79790 to AAC79798 and  
CC AAB44761 represent sequences used in the exemplification of the present  
CC invention.

AA	Sequence	86 AA;
S0		

Query Match 51.2%; Score 43; DB 21; Length 86;  
Best Local Similarity 53.3%; Pred. NO. 5;  
Matches 8; Conservative 3; Mismatches 4; Indels

```
QY      1 LATRLMKKFKA EIRD 15
        |||| :| ||| : :
rb      67 latrlksfkanlen 81
```

RESULT 7  
AAB44823  
ID AAB44823 standard: Protein: 86 AA.

XX  
AC

12-FEB-2001 (first entry)

Human secreted protein sequence encoded by gene 36 SEQ ID NO:122.

XX  
DE  
DA  
XX  
XX  
KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;  
KW antirheumatic; antiproliferative; cytostatic; cardiac; vasotropic;  
KW cerebroprotective; nontropic; neuroprotective; antibacterial; virucide;  
KW fungicide; ophthalmological; gene therapy; autoimmune disease; infection;  
KW hyperproliferative disorder; cardiovascular disorder; angogenesis;  
KW cerebrovascular disorder; nervous system disorder; ocular disorder;  
KW antineoplastic; bisecting; food additive; preservative.

AA Homo sapiens.

AA WO200058336-A1.  
PN

05-OCT-2000.

23-MAR-2000: 2000WO-US07726.

XX  
PR 26-MAR-1999: 99US-0126597.

PR 07-JAN-2000, 2000003 017-1077:  
XX

PA (HUMAN) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA Ruben SM. Komatsoulis G:

XX  
DP  
WPT: 2000-602355/57.

XX Nucleic acid encoding human secreted proteins, used to treat, prevent,  
PT ameliorate or diagnose medical conditions such as cancer, and  
PT autoimmune diseases -  
PT

XX Disclosure: Page 381; 391pp; English.  
PS

The polynucleotide sequences given in AAC79799 to AAC79848 encode the human secreted proteins given in AB44762 to AB94811. AB94812 to AB44829 represent human secreted polypeptide sequences and proteins homologous to them, which are used in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities are: immunosuppressive; antiarthritic; antirheumatic; antiproliferative; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiac; vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial; virocidic; fungicide; and ophthalmological. The polynucleotides and polypeptides can be used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases, hyperproliferative disorders, cardiovascular

CC disorders, cerebrovascular disorders, angiogenesis, nervous system  
CC disorders, infections caused by bacteria, viruses and fungi and ocular  
CC disorders. The polypeptides can also be used to aid wound healing and  
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to  
CC maintain organs before transplantation, for supporting cell culture of  
CC primary tissues, to regenerate tissues and in chemotaxis. The  
CC polypeptides can also be used as a food additive or preservative to  
CC increase or decrease storage capabilities. AAC79790 to AAC79798 and  
CC AAB44761 represent sequences used in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 86 AA;

Query Match 51.2%; Score 43; DB 21; Length 86;  
Best Local Similarity 53.3%; Pred. No. 5;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LATRLMKKFKAEIRD 15  
||||:| ||| : :  
Db 67 latrflksfkanlen 81

RESULT 8  
AAB57133  
ID AAB57133 standard; Protein; 98 AA.

XX AAB57133;

XX 13-MAR-2001 (first entry)

DE Human prostate cancer antigen protein sequence SEQ ID NO:1711.

XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;  
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;  
KW vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;  
KW antibacterial; gene therapy; neural; immune; reproductive; renal;  
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
KW wound; infectious disease.

XX Homo sapiens.

XX WO200055174-A1.

XX 21-SEP-2000.

PF 08-MAR-2000; 2000WO-US05988.

XX 12-MAR-1999; 99US-0124270.

XX (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.

XX Rosen CA, Ruben SM;

XX WPI; 2000-587513/55.

DR N-PSDB; AAF16336.

PT Prostate cancer associated gene sequences, referred to as prostate  
PT cancer antigens, useful for treatment, prevention, and diagnosis of  
PT disorders such as prostate cancer.

XX Claim 11; Page 2184; 2338pp; English.

XX AAF15566 to AAF16505 encode the human prostate cancer associated  
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.  
CC The prostate cancer antigens can have neuroprotective, cytostatic,  
CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,  
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,  
CC and can be used in gene therapy. The prostate cancer antigen  
CC polynucleotides may be used for detection of prostate cancer, chromosome  
CC identification, as chromosome markers, and for numerous other diagnostic  
CC or research purposes. The prostate cancer antigens may be used to treat

CC disorders such as neural, immune, muscular, reproductive,  
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative  
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to  
CC AAB57303 represent sequences used in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 98 AA;

Query Match 51.2%; Score 43; DB 21; Length 98;  
Best Local Similarity 53.3%; Pred. No. 5.7;  
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KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
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KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
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Search completed: January 29, 2002, 10:59:19  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 10:59:57 ; Search time 32.24 Seconds  
(without alignments)  
11.866 Million cell updates/sec

Title: US-09-763-397A-23

Perfect score: 84

Sequence: 1 LATRLMKFKFAEIRDF 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

- 1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Query	Score	Match	Length	DB	ID	Description
1	41	48.8	2325	3	US-08-417-089-6		Sequence 6, Appli
2	41	48.8	2325	4	US-08-695-651-6		Sequence 6, Appli
3	41	48.8	2325	4	US-08-930-285-6		Sequence 6, Appli
4	41	48.8	2325	4	US-08-695-421-6		Sequence 6, Appli
5	40	47.6	775	1	US-07-603-133B-15		Sequence 15, Appl
6	40	47.6	775	1	US-07-603-133B-16		Sequence 16, Appl
7	39	46.4	1147	3	US-08-470-260-5		Sequence 5, Appli
8	39	46.4	1147	3	US-08-471-491-5		Sequence 5, Appli
9	39	46.4	1147	4	US-08-466-662-5		Sequence 5, Appli
10	39	46.4	3289	2	US-08-477-451-2		Sequence 2, Appli
11	37	44.0	306	1	US-08-089-986-2		Sequence 2, Appli
12	37	44.0	306	1	US-08-478-585-2		Sequence 2, Appli
13	37	44.0	306	1	US-08-717-312-2		Sequence 2, Appli
14	37	44.0	306	2	US-08-266-408-2		Sequence 2, Appli
15	37	44.0	306	5	PCT-US94-07886-2		Sequence 2, Appli
16	37	44.0	776	1	US-07-603-133B-18		Sequence 18, Appl
17	37	44.0	859	1	US-08-053-614-2		Sequence 2, Appli
18	37	44.0	859	1	US-08-316-377B-2		Sequence 2, Appli
19	37	44.0	859	2	US-09-034-306-2		Sequence 2, Appli
20	37	44.0	859	4	US-09-259-437-2		Sequence 2, Appli
21	37	44.0	859	5	PCT-US93-09782-2		Sequence 2, Appli
22	37	44.0	1181	1	US-08-053-614-4		Sequence 4, Appli
23	37	44.0	1181	1	US-08-316-377B-4		Sequence 4, Appli
24	37	44.0	1181	2	US-09-034-306-4		Sequence 4, Appli
25	37	44.0	1181	4	US-09-259-437-4		Sequence 4, Appli
26	37	44.0	1181	5	PCT-US93-09782-4		Sequence 4, Appli
27	37	44.0	1784	4	US-09-040-738-2		Sequence 2, Appli

28	37	44.0	1784	4	US-08-652-426A-2	Sequence 2, Appli
29	35	41.7	20	1	US-08-311-611A-57	Sequence 57, Appl
30	35	41.7	20	1	US-08-311-611A-150	Sequence 150, App
31	35	41.7	20	1	US-08-372-783-57	Sequence 57, Appl
32	35	41.7	20	1	US-08-372-783-150	Sequence 150, App
33	35	41.7	20	1	US-08-372-105-57	Sequence 57, Appl
34	35	41.7	20	1	US-08-372-105-150	Sequence 150, App
35	35	41.7	20	1	US-08-306-473A-57	Sequence 57, Appl
36	35	41.7	20	1	US-08-306-473A-150	Sequence 150, App
37	35	41.7	20	1	US-08-209-762-57	Sequence 57, Appl
38	35	41.7	20	2	US-08-621-803-47	Sequence 47, Appl
39	35	41.7	20	2	US-08-485-445A-57	Sequence 57, Appl
40	35	41.7	20	2	US-08-485-445A-150	Sequence 150, App
41	35	41.7	20	3	US-09-119-263-57	Sequence 57, Appl
42	35	41.7	20	3	US-09-119-263-150	Sequence 150, App
43	35	41.7	20	4	US-08-657-162-57	Sequence 57, Appl
44	35	41.7	20	4	US-08-657-162-150	Sequence 150, App
45	35	41.7	20	4	US-09-224-480-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1  
US-08-417-089-6  
; Sequence 6, Application US/08417089  
; Patent No. 6069298  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: METHODS AND AN ACETYL COA CARBOXYLASE GENE  
; TITLE OF INVENTION: FOR CONFERRING HERBICIDE TOLERANCE AND AN ALTERATION IN  
; TITLE OF INVENTION: OIL CONTENT OF PLANTS  
; NUMBER OF SEQUENCES: 11  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION NUMBER: US/08/417,089  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2325 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-417-089-6

Query Match 48.8%; Score 41; DB 3; Length 2325;  
Best Local Similarity 53.3%; Pred. No. 1.1e+02;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LATRLMKFKFAEIR 15  
Db 919 LATRLPRNLKSELED 933

RESULT 2  
US-08-695-651-6  
; Sequence 6, Application US/08695651  
; Patent No. 6146867  
; GENERAL INFORMATION:  
; APPLICANT: Gengenbach, B. G.  
; APPLICANT: Somers, D. A.  
; APPLICANT: Wyse, D. L.  
; APPLICANT: Gronwald, J. W.  
; APPLICANT: Egli, M. A.  
; APPLICANT: Lutz, S. M.  
; TITLE OF INVENTION: METHOD FOR PRODUCING PLANT ACETYL COA  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.  
STREET: P.O. Box 2938  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/695,651  
FILING DATE: 12-AUG-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/417089  
FILING DATE: 05-APR-1995  
APPLICATION NUMBER: 08/014326  
FILING DATE: 05-FEB-1993  
APPLICATION NUMBER: 07/917462  
FILING DATE: 21-JUL-1992  
APPLICATION NUMBER: 07/538674  
FILING DATE: 18-JUN-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Woessner, Warren D  
REGISTRATION NUMBER: 30,440  
REFERENCE/DOCKET NUMBER: 600.318US3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-373-6900  
TELEFAX: 612-339-3061  
TELEX:

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2325 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: N-terminal  
US-08-695-651-6

Query Match 48.8%; Score 41; DB 4; Length 2325;  
Best Local Similarity 53.3%; Pred. No. 1.1e+02;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LATRLMKKFKAEIRD 15  
||||| :|:|:|

Db 919 LATRLPRNLKSELED 933

RESULT 3  
US-08-930-285-6  
Sequence 6, Application US/08930285  
Patent No. 6222099  
GENERAL INFORMATION:

APPLICANT: Regents of the University of Minnesota, et al.  
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING ACETYL COA CARBOXYLASE GE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.  
STREET: P. O. Box 2938  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/930,285  
FILING DATE: 13-APR-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/04625  
FILING DATE: 04-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Embretson, Janet E.  
REGISTRATION NUMBER: 39,665  
REFERENCE/DOCKET NUMBER: 600.318US4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-339-0331  
TELEFAX: 612-339-3061  
TELEX:

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2325 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal and C-terminal (full length protein)  
ORIGINAL SOURCE:  
US-08-930-285-6

Query Match 48.8%; Score 41; DB 4; Length 2325;  
Best Local Similarity 53.3%; Pred. No. 1.1e+02;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LATRLMKKFKAEIRD 15  
||||| :|:|:|

Db 919 LATRLPRNLKSELED 933

RESULT 4  
US-08-695-421-6  
Sequence 6, Application US/08695421  
Patent No. 6268550  
GENERAL INFORMATION:  
APPLICANT: Gengenbach, B. G.  
APPLICANT: Somers, D. A.  
APPLICANT: Wyse, D. L.  
APPLICANT: Gronwald, J. W.  
APPLICANT: Egli, M. A.  
APPLICANT: Lutz, S. M.  
TITLE OF INVENTION: METHODS AND AN ACETYL COA CARBOXYLASE GENE  
TITLE OF INVENTION: FOR CONFERRING HERBICIDE TOLERANCE AND AN ALTERATION IN OIL  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.  
STREET: P.O. Box 2938  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/695,421  
FILING DATE: 23-AUG-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/417089  
FILING DATE: 05-APR-1995  
APPLICATION NUMBER: 08/014326  
FILING DATE: 05-FEB-1993  
APPLICATION NUMBER: 07/917462



;; FILING DATE: 21-JUL-1992  
;; APPLICATION NUMBER: 07/538674  
;; FILING DATE: 18-JUN-1990  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Woessner, Warren D  
;; REGISTRATION NUMBER: 30,440  
;; REFERENCE/DOCKET NUMBER: 600.318US2  
;; TELEPHONE: 612-373-6900  
;; TELEFAX: 612-339-3061  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2325 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; FRAGMENT TYPE: N-terminal  
;; US-08-695-421-6

Query Match 48.8%; Score 41; DB 4; Length 2325;  
Best Local Similarity 53.3%; Pred. No. 1.1e+02;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 LATRLMKKFAEIRD 15  
      ||||| : 1:1: |  
Db 919 LATRLPRNLKSELD 933

RESULT 5  
US-07-603-133B-15  
; Sequence 15, Application US/07603133B  
; Patent No. 5298244  
; GENERAL INFORMATION:  
; APPLICANT: Redmond, Mark J.  
; APPLICANT: Ijaz, Mohammed K.  
; TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR  
; TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 545 Middlefield Road, Suite 200  
; CITY: Menlo Park  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 19901025  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Robins, Roberta L.  
; REGISTRATION NUMBER: 33,208  
; REFERENCE/DOCKET NUMBER: 9313-0004.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 327-7250  
; TELEFAX: (415) 327-2951  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 775 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein

US-07-603-133B-15

Query Match 47.6%; Score 40; DB 1; Length 775;  
Best Local Similarity 70.0%; Pred. No. 55;  
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LATRLMKKFK 10  
      :|||||  
Db 543 MATKVMKKFK 552

RESULT 6  
US-07-603-133B-16  
; Sequence 16, Application US/07603133B  
; Patent No. 5298244  
; GENERAL INFORMATION:  
; APPLICANT: Redmond, Mark J.  
; APPLICANT: Ijaz, Mohammed K.  
; APPLICANT: Parker, Michael D.  
; TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR  
; TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 545 Middlefield Road, Suite 200  
; CITY: Menlo Park  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC-compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/603.133B  
; FILING DATE: 19901025  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Robins, Roberta L.  
; REGISTRATION NUMBER: 33,208  
; REFERENCE/DOCKET NUMBER: 9313-0004.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 327-7250  
; TELEFAX: (415) 327-2951  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 775 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; US-07-603-133B-16

Query Match 47.6%; Score 40; DB 1; Length 775;  
Best Local Similarity 70.0%; Pred. No. 55;  
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LATRLMKKFK 10  
      :|||||  
Db 543 MATKVMKKFK 552

RESULT 7  
US-08-470-260-5  
; Sequence 5, Application US/08470260  
; Patent No. 6077706  
; GENERAL INFORMATION:  
; APPLICANT: Covacci, Antonello  
; APPLICANT: Bugnoli, Massimo

APPLICANT: Telford, John  
APPLICANT: Macchia, Giovanni  
APPLICANT: Rappuoli, Rino  
TITLE OF INVENTION: Helicobacter Pylori Proteins Useful  
for Vaccines and Diagnostics  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/470,260  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/256,848  
FILING DATE: 21-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: McClung, Barbara G.  
REGISTRATION NUMBER: 33,113  
REFERENCE/DOCKET NUMBER: 0316.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 501-2708  
TELEFAX: (510) 653-3342  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1147 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-470-260-5

Query Match 46.4%; Score 39; DB 3; Length 1147;  
Best Local Similarity 43.8%; Pred. No. 1.2e+02;  
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 LATRLMKKFAEIRDF 16  
| : : ||: ||: ||  
DB 413 LSEKEKEKFRTEIKDF 428

RESULT 8  
US-08-471-491-5  
; Sequence 5, Application US/08471491B  
; Patent No. 6090611  
; GENERAL INFORMATION:  
; APPLICANT: Covacci, Antonello  
; APPLICANT: Bugnoli, Massimo  
; APPLICANT: Telford, John  
; APPLICANT: Macchia, Giovanni  
; APPLICANT: Rappuoli, Rino  
; TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And  
; FILE REFERENCE: CHIR004  
; CURRENT APPLICATION NUMBER: US/08/471,491B  
; CURRENT FILING DATE: 1995-06-06  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 1147  
; TYPE: PRT  
; ORGANISM: Helicobacter pylori  
US-08-471-491-5

Query Match 46.4%; Score 39; DB 3; Length 1147;  
Best Local Similarity 43.8%; Pred. No. 1.2e+02;  
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 LATRLMKKFAEIRDF 16  
| : : ||: ||: ||  
DB 413 LSEKEKEKFRTEIKDF 428

RESULT 9  
US-08-466-662-5  
; Sequence 5, Application US/08466662B  
; Patent No. 6130059  
; GENERAL INFORMATION:  
; APPLICANT: Covacci, Antonello  
; APPLICANT: Bugnoli, Massimo  
; APPLICANT: Telford, John  
; APPLICANT: Macchia, Giovanni  
; APPLICANT: Rappuoli, Rino  
; TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And  
; FILE REFERENCE: CHIR0057  
; CURRENT APPLICATION NUMBER: US/08/466,662B  
; CURRENT FILING DATE: 1995-06-06  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 1147  
; TYPE: PRT  
; ORGANISM: Helicobacter pylori  
US-08-466-662-5

Query Match 46.4%; Score 39; DB 4; Length 1147;  
Best Local Similarity 43.8%; Pred. No. 1.2e+02;  
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 LATRLMKKFAEIRDF 16  
| : : ||: ||: ||  
DB 413 LSEKEKEKFRTEIKDF 428

RESULT 10  
US-08-477-451-2  
; Sequence 2, Application US/08477451  
; Patent No. 5928865  
; GENERAL INFORMATION:  
; APPLICANT: Covacci, Antonello  
; TITLE OF INVENTION: Helicobacter Pylori Cagi Region  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation  
; STREET: 4560 Horton Street  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,451  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McClung, Barbara G.  
; REGISTRATION NUMBER: 33,113  
; REFERENCE/DOCKET NUMBER: 0335.002  
; TELECOMMUNICATION INFORMATION:



Db 28 LHTKTLKEYTSDLKDF 43

RESULT 15

PCT-US94-07886-2

Sequence 2, Application PC/TUS9407886

GENERAL INFORMATION:

APPLICANT: Baum, James A.

TITLE OF INVENTION: Bacillus thuringiensis Transposon Tn5401

TITLE OF INVENTION: and its use in a Site-Specific Recombination System For

TITLE OF INVENTION: Recombinant Bacillus thuringiensis Strain Development

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: Panitch Schwarze Jacobs & Nadel c/o A.S. Nadel

STREET: 1601 Market Street, 36th Floor

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM: disk

MEDIUM TYPE: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/07886

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/089,986

FILING DATE: 08-JUL-1993

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 306 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US94-07886-2

Query Match 44.0%; Score 37; DB 5; Length 306;

Best Local Similarity 31.2%; Pred. No. 68;

Matches 5; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 LATRLMKKFKAEIRDF 16

Db 28 LHTKTLKEYTSDLKDF 43

Search completed: January 29, 2002, 10:59:58

Job time: 2144 sec

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/717,312

FILING DATE: 20-SEP-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/266,408

FILING DATE: 24-JUL-1994

APPLICATION NUMBER: US 08/089,986

FILING DATE: 08-JUL-1993

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 306 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-717-312-2

Query Match 44.0%; Score 37; DB 1; Length 306;

Best Local Similarity 31.2%; Pred. No. 68;

Matches 5; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 LATRLMKKFKAEIRDF 16

Db 28 LHTKTLKEYTSDLKDF 43

RESULT 14

US-08-266-408-2

Sequence 2, Application US/08266408

Patent No. 5843744

GENERAL INFORMATION:

APPLICANT: Baum, James A.

TITLE OF INVENTION: Bacillus thuringiensis Transposon Tn5401

TITLE OF INVENTION: and its use in a Site-Specific Recombination System For

TITLE OF INVENTION: Recombinant Bacillus thuringiensis Strain Development

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: Panitch Schwarze Jacobs & Nadel c/o A.S. Nadel

STREET: 1601 Market Street, 36th Floor

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM: disk

MEDIUM TYPE: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/266,408

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/089,986

FILING DATE: 08-JUL-1993

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 306 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-266-408-2

Query Match 44.0%; Score 37; DB 2; Length 306;

Best Local Similarity 31.2%; Pred. No. 68;

Matches 5; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 LATRLMKKFKAEIRDF 16

er

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model  
Run on: January 29, 2002, 11:00:39 ; Search time 34.94 Seconds  
(without alignments)  
37.063 Million cell updates/sec

Title: US-09-763-397A-23  
Perfect score: 84  
Sequence: 1 LATRLMKKFAEIRDF 17  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues  
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	782	2	S27833
2	43	51.2	227	2	B82902
3	43	51.2	353	2	T05552
4	42	50.0	141	2	A32124
5	42	50.0	346	2	S73894
6	42	50.0	398	2	F85056
7	42	50.0	456	2	B71135
8	42	50.0	496	2	T52255
9	42	50.0	743	2	C86168
10	41	48.8	319	2	H84808
11	41	48.8	503	2	T52172
12	41	48.8	619	2	D69318
13	41	48.8	1530	1	S01393
14	41	48.8	1625	2	T02921
15	41	48.8	1685	2	T02750
16	41	48.8	2325	2	T02235
17	40	47.6	302	2	H83478
18	40	47.6	346	2	G86305
19	40	47.6	356	2	T05551
20	40	47.6	527	2	H85230
21	40	47.6	535	2	T03246
22	40	47.6	535	2	T03260
23	40	47.6	568	2	S12755
24	40	47.6	774	1	VPXRWT
25	40	47.6	775	1	VPXRW7
26	40	47.6	776	1	VPXRW9
27	40	47.6	1206	2	D84542
28	39	46.4	268	2	F71712
29	39	46.4	344	2	C70388

30	39	46.4	358	2	S44261
31	39	46.4	429	2	G84176
32	39	46.4	511	2	S40411
33	39	46.4	601	2	G71666
34	39	46.4	776	2	A48480
35	39	46.4	986	2	S49394
36	39	46.4	1215	2	B48281
37	39	46.4	2105	1	A44059
38	38	45.2	230	2	A83362
39	38	45.2	235	2	E86127
40	38	45.2	337	2	T06720
41	38	45.2	397	2	JH0416
42	38	45.2	398	2	F64456
43	38	45.2	509	2	A35016
44	38	45.2	541	2	S40412
45	38	45.2	547	2	S41618

ALIGNMENTS

RESULT 1  
S27833  
rhothy-associated protein 1 precursor - malaria parasite (Plasmodium falciparum)  
N:Alternate names: protective antigen  
C:Species: Plasmodium falciparum  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jun-2000  
C:Accession: A45514; S27833  
R:Ridley, R.G.; Takacs, B.; Lahm, H.W.; Delves, C.J.; Goman, M.; Certa, U.; Matile, H. Mol. Biochem. Parasitol. 41, 125-134, 1990  
A:Title: Characterisation and sequence of a protective rhothy antigen from Plasmodium falciparum  
A:Reference number: A45514; MUID:90348711  
A:Accession: A45514  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-782 <RI2>  
A:Cross-references: GB:M32853; NID:gl60656; PID:gl60657  
C:Superfamily: Plasmodium falciparum rhothy-associated protein 1

Query Match 100.0%; Score 84; DB 2; Length 782;  
Best Local Similarity 100.0%; Pred. No. 8e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LATRLMKKFAEIRDF 17  
DB 736 LATRLMKKFAEIRDF 752

RESULT 2  
B82902  
tRNA pseudouridine 55 synthase U0354 [imported] - Ureaplasma urealyticum  
C:Species: Ureaplasma urealyticum  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: B82902  
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000  
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a  
A:Reference number: A82870  
A:Accession: B82902  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-237 <GLA>  
A:Cross-references: GB:AE002132; GB:AF222894; NID:g6899327; PIDN:AAF30763.1; GSPDB:GN  
A:Experimental source: serovar 3; biovar 1  
C:Genetics:  
A:Gene: trbB; U0354  
A:Genetic code: SGC3

Query Match 51.2%; Score 43; DB 2; Length 227;  
Best Local Similarity 56.2%; Pred. No. 11;  
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LATRLMKKFKAEIRDF 16  
: | | | | : | | |  
Db 143 IAPRLVKIKYQIMDF 158

RESULT 3  
SRG1 protein-related protein F24A6.150 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 23-Jul-1999  
C:Accession: T05552  
R:Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.  
submitted to the Protein Sequence Database, February 1999  
A:Reference number: Z15419  
A:Accession: T05552  
A:Molecule type: DNA  
A:Residues: 1-353 <BEV>  
A:Cross-references: EMBL:AL035396  
A:Experimental source: cultivar Columbia; BAC clone F24A6  
C:Genetics:  
A:Map position: 4  
A:Introns: 84/3; 164/2; 273/3  
A:Note: F24A6.150  
C:Superfamily: 1-aminocyclopropane-1-carboxylate oxidase

Query Match 51.2%; Score 43; DB 2; Length 353;  
Best Local Similarity 58.3%; Pred. No. 18;  
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 MKKFKAEIRDF 17  
: | | | | : | | |  
Db 92 LDKFKSDIQDF 103

RESULT 4  
A32124  
photosystem I chain II - Synechocystis sp. (strain PCC 6803)  
N:Alternate names: photosystem I reaction center chain II  
C:Species: Synechocystis sp.  
A:Variety: PCC 6803  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 20-Jun-2000  
C:Accession: A32124; S74536; S67980  
R:Reilly, P.; Hulmes, J.D.; Pan, Y.C.E.; Nelson, N.  
J. Biol. Chem. 263, 17658-17662, 1988  
A:Title: Molecular cloning and sequencing of the psad gene encoding subunit II of photos  
A:Reference number: A92692; MUID:89034300  
A:Accession: A32124  
A:Molecule type: DNA  
A:Residues: 1-141 <REI>  
A:Cross-references: GB:J04195; NID:g154480; PIDN:AAA88625.1; PID:g154481  
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
DNA Res. 3, 109-136, 1996  
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis  
s.  
A:Reference number: S74322; MUID:97061201  
A:Accession: S74536  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-141 <KAN>  
A:Cross-references: EMBL:D90899; GB:AB001339; NID:g1651650; PIDN:BAAL16688.1; PID:g165176  
R:Barbato, R.; Polverino de Laureto, P.; Rigoni, F.; de Martini, E.; Giacometti, G.M.  
Eur. J. Biochem. 234, 459-465, 1995  
A:Title: Pigment-protein complexes from the photosynthetic membrane of the cyanobacteriu  
A:Reference number: S67978; MUID:96128174  
A:Accession: S67980  
A:Molecule type: protein  
A:Residues: 2, 'S', '4-9, 'L', 11-13 <BAR>  
C:Genetics:  
A:Gene: psad

C:Superfamily: photosystem I chain II

Query Match 50.0%; Score 42; DB 2; Length 141;  
Best Local Similarity 50.0%; Pred. No. 11;  
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 LATRLMKKFKAEIRDF 16  
: | | | | : | | |  
Db 68 LGTQLTKFKPKIQDY 83

RESULT 5  
S73894  
tryptophan--trna ligase (EC 6.1.1.2) trps - Mycoplasma pneumoniae (strain ATCC 29342)  
N:Alternate names: hypothetical protein A65\_orf346; tryptophanyl-trna synthetase trps  
C:Species: Mycoplasma pneumoniae  
A:Variety: ATCC 29342  
C:Date: 27-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 07-Dec-1999  
C:Accession: S73894  
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.  
Nucleic Acids Res. 24, 4420-4449, 1996  
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumonia  
A:Reference number: S73327; MUID:97105885  
A:Accession: S73894  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-346 <HIM>  
A:Cross-references: EMBL:AE000056; GB:U00089; NID:g1674263; PIDN:AAB96216.1; PID:g167  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
C:Genetics:  
A:Gene: trps  
A:Genetic code: SGC3  
C:Superfamily: tryptophan--trna ligase  
C:Keywords: aminoacyl-trna synthetase; ligase; protein biosynthesis

Query Match 50.0%; Score 42; DB 2; Length 346;  
Best Local Similarity 57.1%; Pred. No. 25;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 LATRLMKKFKAEIR 14  
: | | | | : | | |  
Db 165 LAQRIQKKFKLKL 178

RESULT 6  
F85056  
hypothetical protein AT4g04480 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 16-Feb-2001  
C:Accession: F85056  
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp  
Nature 402, 769-777, 1999  
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A:Reference number: A85001; MUID:20083488  
A:Accession: F85056  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-398 <STO>  
A:Cross-references: GB:NC\_001268; NID:g7267205; PIDN:CAB77916.1; GSPDB:GN00140  
C:Genetics:  
A:Gene: AT4g04480  
A:Map position: 4

Query Match 50.0%; Score 42; DB 2; Length 398;  
Best Local Similarity 60.0%; Pred. No. 29;  
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATRLMKKFKAEIRDF 16  
: | | | | : | | |  
Db 165 ATRLFKKLRLVEIMF 179



```
RESULT 7
B71135
hypothetical protein PH0846 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C:Accession: B71135
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137
A:Accession: B71135
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-456 <KAW>
A:Cross-references: GB:AP000003; NID:g3236130; PIDN:BAA29940.1; PID:g3257257
A:Experimental source: strain OT3
A:Note: This accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0846
C:Superfamily: Methanobacterium thermoautotrophicum conserved hypothetical protein MTH19

Query Match 50.0%; Score 42; DB 2; Length 456;
Best Local Similarity 53.3%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TRLMKFKAEIRDF 17
|||||: |||
Db 35 TRLAEFSKDKRTFF 49

RESULT 8
T52255
cytochrome P450 [imported] - Thlaspi arvense
C:Species: Thlaspi arvense
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 16-Feb-2001
C:Accession: T52255
R:Udvardi, M.K.; Metzger, J.D.; Krishnapillai, V.; Peacock, W.J.; Dennis, E.S.
Plant Physiol. 104, 755-756, 1994
A:Title: Cloning and nucleotide sequence of a full-length cDNA from Thlaspi arvense that
A:Reference number: Z26005
A:Accession: T52255
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-496 <UDV>
A:Cross-references: EMBL:L24438; PIDN:AAAL19701.1
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: heme; iron; metalloprotein
F:294-458/Domain: cytochrome P450 homology <P45>
F:436/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 50.0%; Score 42; DB 2; Length 496;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 RLMKKFKAEIRD 15
|||||: |||
Db 318 RVMKKLQAEIRE 329

RESULT 9
C86168
hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: C86168
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizlar, L.
```

```
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maity, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: C86168
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-743 <STO>
A:Cross-references: GB:AE005172; NID:g4204309; PIDN:AAD10690.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 50.0%; Score 42; DB 2; Length 743;
Best Local Similarity 61.5%; Pred. No. 52;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 LMKKFKAEIRDF 17
|||||: |||
Db 285 LMKKFKTSTRDLF 297

RESULT 10
H84808
probable annexin [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: H84808
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, D.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: H84808
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-319 <STO>
A:Cross-references: GB:AE002093; NID:g3785997; PIDN:AAC67343.1; GSPDB:GN00139
C:Genetics:
A:Gene: AT2g38750
A:Map position: 2

Query Match 48.8%; Score 41; DB 2; Length 319;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LATRLMKFKAEIRDF 16
|||: |||
Db 295 LAQRIQEKIGNYRDF 310

RESULT 11
T52172
probable cytochrome P450 At2g24180 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 16-Feb-2001
C:Accession: T52172; E84633
R:Mizutani, M.; Ward, E.; Ohta, D.
Plant Mol. Biol. 37, 39-52, 1998
A:Title: Cytochrome p450 superfamily in Arabidopsis thaliana: isolation of cDNAs, dif
A:Reference number: Z14382; MUID:98281573
A:Accession: T52172
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-503 <MIT>
A:Cross-references: EMBL:D78604; PIDN:BAA28536.1
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
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Db 279 LATRLPRNLKSELED 293  
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Job time: 2030 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 29, 2002, 11:16:19 ; Search time 20.36 Seconds  
(without alignments)  
30.614 Million cell updates/sec

Title: US-09-763-397A-23

Perfect score: 84

Sequence: 1 LATRLMKFKAEIRDF 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	43	51.2	227	1	TRUB_UREPA	O9pqd7 ureaplasma
2	43	51.2	501	1	ODPX_HUMAN	O00330 homo sapien
3	42	50.0	140	1	PSAD_SYNY3	P19569 synchocyst
4	42	50.0	346	1	SYW_MYCPN	P75510 mycoplasma
5	42	50.0	496	1	C7B1_THLAR	P49264 thlaspi arv
6	41	48.8	503	1	C726_ARATH	O65787 arabidopsis
7	41	48.8	619	1	SYT_ARCFU	O23703 archaeglob
8	41	48.8	1530	1	RPC1_TRYBB	P08968 trypanosoma
9	40	47.6	194	1	YMP9_CAEEL	O10952 caenorhabdi
10	40	47.6	500	1	C72Q_ARATH	O91t10 arabidopsis
11	40	47.6	535	1	C7C3_MAI2E	P93703 zea mays (m
12	40	47.6	774	1	VP4_ROTHT	P11200 human rotav
13	40	47.6	775	1	VP4_ROTTH	P11197 human rotav
14	40	47.6	776	1	VP4_ROTTH	P11199 human rotav
15	39	46.4	268	1	LGT_RICRP	O9ze99 rickettsia
16	39	46.4	344	1	YA22_AQUAE	O67134 aquifex aeo
17	39	46.4	429	1	DHE4_HALN1	O9bsm4 halobacteri
18	39	46.4	496	1	C72B_ARATH	P58049 arabidopsis
19	39	46.4	496	1	C72D_ARATH	P58050 arabidopsis
20	39	46.4	496	1	C72E_ARATH	P58051 arabidopsis
21	39	46.4	511	1	AROF_LYCES	P37215 lycopersico
22	39	46.4	1147	1	CGA1_HELPY	P80200 helicobacte
23	39	46.4	2105	1	POLR_ASGVP	P36309 apple stem
24	38	45.2	397	1	FTU_MYCHO	P22679 mycoplasma
25	38	45.2	502	1	C72G_ARATH	O91tm7 arabidopsis
26	38	45.2	538	1	AROF_SOLTU	P21357 solanum tub
27	38	45.2	541	1	AROF_LYCES	P37216 lycopersico
28	38	45.2	542	1	AROF_TOBAC	P27608 nicotiana t
29	38	45.2	775	1	VP4_ROTGP	P23045 porcine rot
30	38	45.2	776	1	VP42_ROTSL	P12976 simian 11 r
31	38	45.2	776	1	VP4_ROTBS	P36305 bovine rota
32	38	45.2	776	1	VP4_ROTDF	O06894 canine rota
33	38	45.2	776	1	VP4_ROTFF	O07416 feline rota

34	38	45.2	776	1	VP4_ROTTH6	P26451 human rotav
35	38	45.2	776	1	VP4_ROTTH	O06895 human rotav
36	38	45.2	776	1	VP4_ROTSS	P17464 simian 11 r
37	37.5	44.6	1323	1	LT23_CAEEL	P24348 caenorhabdi
38	37	44.0	187	1	RL5_MYCTU	P95064 mycobacteri
39	37	44.0	189	1	YNO0_YEAST	P53910 saccharomyc
40	37	44.0	244	1	RHOE_HUMAN	P52199 homo sapien
41	37	44.0	244	1	RHOE_PIG	O77683 sus scrofa
42	37	44.0	263	1	TRUA_PYRAB	Q9uz23 pyrococcus
43	37	44.0	322	1	ACCL_ORYSA	O40634 oryza sativ
44	37	44.0	329	1	NUC1_YEAST	P08466 saccharomyc
45	37	44.0	347	1	SYW_MYCGE	P47372 mycoplasma

ALIGNMENTS

```
RESULT 1
TRUB_UREPA
ID TRUB_UREPA STANDARD; PRT; 227 AA.
AC Q9POD7: 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 5S
DE SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL
DE HYDROLYASE).
GN TRUB OR UU354.
OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Ureaplasma.
OX NCBI_TaxID=134821;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SEROVAR 3;
RX MEDLINE=20500219; PubMed=11048724;
RA Glass J.I., Lefkowitz E.J., Glass J.S., Helner C.R., Chen E.Y.,
RA Casseil G.H.;
RT "The complete sequence of the mucosal pathogen Ureaplasma
urealyticum."
RT Nature 407:757-762(2000).
CC -!- FUNCTION: FORMATION OF PSEUDOURIDINE AT POSITION 55 IN THE
CC PSI GC LOOP OF TRANSFER RNAS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: URACIL + D-RIBOSE 5-PHOSPHATE -> PSEUDOURIDINE
CC 5'-PHOSPHATE + H(2)O.
CC -!- SIMILARITY: BELONGS TO THE TRUB FAMILY OF PSEUDOURIDINE SYNTHASES.
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CC -----
CC EMBL: AE002132; AAF30763.1; -
CC InterPro: IPR002501; TruB_N.
CC Pfam: PF01509; TruB_N; 1
CC Lyase; TRNA processing; Complete proteome.
SQ SEQUENCE 227 AA; 25765 MW; FA1CADC357D6AD36 CRC64;
```

Query Match 51.2%; Score 43; DB 1; Length 227;  
Best Local Similarity 56.2%; Pred. No. 3.7;  
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LATRLMKFKAEIRDF 16  
: ||: ||: ||  
Db 143 IAPRLVKFKYQIMDF 158

RESULT 2  
ODPX\_HUMAN

ID ODPX\_HUMAN STANDARD; PRT; 501 AA.  
AC 000330; 099783; 060221;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 20-AUG-2001 (Rel. 40, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE PYRUVATE DEHYDROGENASE PROTEIN X COMPONENT, MITOCHONDRIAL PRECURSOR  
DE (DIHYDROLIPOAMIDE DEHYDROGENASE-BINDING PROTEIN OF PYRUVATE  
DE DEHYDROGENASE COMPLEX) (E3-BINDING PROTEIN) (E3BP) (PROX).  
GN PDX1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97390399; PubMed=9242632;  
RA Harris R.A., Bowker-Kinley M.M., Wu P., Jeng J., Popov K.M.;  
RT "Dihydrolipoamide dehydrogenase-binding protein of the human pyruvate  
RT dehydrogenase complex. DNA-derived amino acid sequence, expression,  
RT and reconstitution of the pyruvate dehydrogenase complex.";  
RL J. Biol. Chem. 272:19746-19751(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=98153629; PubMed=9399911;  
RA Aral B., Benelli C., Ait-Ghezala G., Amessou M., Fouque F.,  
RA Maunoury C., Creau N., Kamoun P., Marsac C.;  
RT "Mutations in PDX1, the human lipoyl-containing component X of the  
RT pyruvate dehydrogenase-complex gene on chromosome 11p1, in congenital  
RT lactic acidosis.";  
RL Am. J. Hum. Genet. 61:1318-1326(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98133932; PubMed=9467010;  
RA Ling M., McEachern G., Seyda A., Mackay N., Scherer S.W.,  
RA Bratinova S., Beatty B., Giovannucci-Uzielli M.L., Robinson B.H.; X  
RT "Detection of a homozygous four base pair deletion in the protein  
RT gene in a case of pyruvate dehydrogenase complex deficiency.";  
RL Hum. Mol. Genet. 7:501-505(1998).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Moore M.;  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 127-501 FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=97264341; PubMed=9110174;  
RA Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,  
RA Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs R.A.;  
RT "Large-scale concatenation cDNA sequencing.";  
RL Genome Res. 7:353-358(1997).  
CC -!- FUNCTION: REQUIRED FOR ANCHORING DIHYDROLIPOAMIDE DEHYDROGENASE  
CC (E3) TO THE DIHYDROLIPOAMIDE TRANSACETYLASE (E2) CORE OF THE  
CC PYRUVATE DEHYDROGENASE COMPLEXES OF EUKARYOTES. THIS SPECIFIC  
CC BINDING IS ESSENTIAL FOR A FUNCTIONAL PDH COMPLEX.  
CC -!- SUBUNIT: EUKARYOTIC PYRUVATE DEHYDROGENASE COMPLEXES ARE ORGANIZED  
CC ABOUT A CORE CONSISTING OF THE OLIGOMERIC DIHYDROLIPOAMIDE ACETYL-  
CC TRANSFERASE, AROUND WHICH ARE ARRANGED MULTIPLE COPIES OF PYRUVATE  
CC DEHYDROGENASE, DIHYDROLIPOAMIDE DEHYDROGENASE AND PROTEIN X BOUND  
CC BY NONCOVALENT BONDS.  
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.  
CC -!- DISEASE: DEFECTS IN PDX1 ARE A CAUSE OF LACTICACIDEMIA.  
CC -!- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.  
CC -!- SIMILARITY: CONTAINS 1 LIPOYL-BINDING DOMAIN.  
CC  
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CC -----

DR EMBL; AF001437; AAB66315.1; -.  
DR EMBL; Y13145; CAA73606.1; -.  
DR EMBL; U82328; AAC39661.1; -.  
DR EMBL; AL138810; CAC12641.1; -.  
DR EMBL; U79296; AAB50223.1; -.  
DR MIM; 245349; -.  
DR InterPro; IPR001078; 2Oxoacid\_dh.  
DR InterPro; IPR000089; Biotin\_lipoyl.  
DR InterPro; IPR003016; Lipoyl.  
DR InterPro; IPR002965; P-rich\_extensn.  
DR Pfam; PF00198; 2-oxoacid\_dh; 1.  
DR Pfam; PF00364; biotin\_lipoyl; 1.  
DR PRINTS; PR01217; PRICHEXTENS. 1.  
DR PRODOM; PD001115; 2Oxoacid\_dh; 1.  
DR PROSITE; PS00189; LIPOYL; 1.  
KW TRANSIT peptide; Mitochondrion; Lipoyl.  
FT TRANSIT 1 53 MITOCHONDRION (BY SIMILARITY).  
FT CHAIN 54 501 PYRUVATE DEHYDROGENASE PROTEIN X  
FT COMPONENT.  
FT BINDING 97 97 LIPOYL (BY SIMILARITY).  
FT CONFLICT 23 23 R -> C (IN REF. 1).  
FT CONFLICT 41 41 A -> R (IN REF. 3).  
FT CONFLICT 251 251 A -> S (IN REF. 1 AND 2).  
SQ SEQUENCE 501 AA; 54122 MW; 9CF0C1DAE9E12EF9 CRC64;  
  
Query Match 51.2%; Score 43; DB 1; Length 501;  
Best Local Similarity 53.3%; Pred. No. 8.4;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 LATRLMKKFKAEIRD 15  
| | | | : | | | : :  
- Db 482 LATRLKSKANLEN 496  
  
RESULT 3  
PSAD\_SYNV3  
ID PSAD\_SYNV3 STANDARD; PRT; 140 AA.  
AC P19569;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE PHOTOSYSTEM I REACTION CENTRE SUBUNIT II (PHOTOSYSTEM I 16 KDA  
DE POLYPEPTIDE) (PSI-D).  
DE PSAD OR SLR0737.  
GN Synechocystis sp. (strain PCC 6803).  
OS Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
OX NCBI\_TaxID=1148;  
[1]  
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.  
RX MEDLINE=89034300; PubMed=3141423;  
RA Reilly P., Hulmes J.D., Pan Y.-C.E., Nelson N.;  
RT "Molecular cloning and sequencing of the psad gene encoding subunit  
RT II of photosystem I from the cyanobacterium, Synechocystis sp. PCC  
RT 6803.";  
RL J. Biol. Chem. 263:17658-17662(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97061201; PubMed=8905231;  
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
RA Miyajima N., Hirose M., Sugita M., Saito S., Kimura T.,  
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,  
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,  
RA Yamada M., Yasuda M., Tabata S.;  
RT "Sequence analysis of the genome of the unicellular cyanobacterium  
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the  
RT entire genome and assignment of potential protein-coding regions.";  
RL DNA Res. 3:109-136(1996).  
CC -!- FUNCTION: PSAD CAN FORM COMPLEXES WITH FERREDOXIN AND FERREDOXIN-  
CC OXIDOREDUCTASE IN PHOTOSYSTEM I (PS I) REACTION CENTRE.  
CC -!- SUBUNIT: PS I FROM SYNECHOCYSTIS SP. CONTAINS SEVEN DIFFERENT  
CC POLYPEPTIDES. THE POLYPEPTIDE CORRESPONDING TO SUBUNIT II FROM  
CC HIGHER PLANTS IS MISSING.  
CC

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CC -!- SIMILARITY: BELONGS TO THE PSAD FAMILY.
CC -----
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CC -----
CC EMBL: J04195; AAA88625.1; .
CC DR EMBL: D90899; BAA16688.1; .
CC DR PIR: A32124; A32124.
CC DR InterPro: IPR003685; Psad.
CC DR Pfam: PF02531; Psad; 1.
CC KW Photosynthesis; Photosystem I; Complete proteome.
CC FT INIT_MET 0
CC SQ SEQUENCE 140 AA; 15513 MW; 263C35D5B47B9F8E CRC64;

Query Match 50.0%; Score 42; DB 1; Length 140;
Best Local Similarity 50.0%; Pred. No. 3.3;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 LATRLMKKFKAEIRDF 16
| | | | | | | |
Db 67 LCTQLRTKFKKIQDY 82

RESULT 4
SYW_MYCPN STANDARD; PRT; 346 AA.
AC P75510.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TRYPTOPHANYL-TRNA SYNTHETASE (EC 6.1.1.2) (TRYPTOPHAN--TRNA LIGASE)
DE (TRPRS).
GN TRPS OR MPN265 OR MP568.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Piagens H., Pirkl E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae."
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -!- CATALYTIC ACTIVITY: ATP + L-TRYPTOPHAN + TRNA(TRP) = AMP +
CC PYROPHOSPHATE + L-TRYPTOPHANYL-TRNA(TRP).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL: AE000056; AAB96216.1; .
CC DR InterPro: IPR002305; tRNA-synt_1b.
CC DR InterPro: IPR001412; tRNA-synt_1.
CC DR Pfam: IPR002306; tRNA-synt_trp.
CC DR Pfam: PF00579; tRNA-synt_1b; 1.
CC DR PRINTS: PR01039; TRNASYNTHTRP.
CC DR PROSITE: PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
```

```
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 11 19 "HIGH" REGION.
FT SITE 200 204 "RMSKS" REGION.
FT BINDING 203 203 ATP (BY SIMILARITY).
SQ SEQUENCE 346 AA; 39079 MW; 56CF4FFCC89C2F95 CRC64;

Query Match 50.0%; Score 42; DB 1; Length 346;
Best Local Similarity 57.1%; Pred. No. 8.4;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 LATRLMKKFKAEIR 14
| | | | | | | |
Db 165 LAQRIQKKFKLKL 178

RESULT 5
C7B1_THLAR STANDARD; PRT; 496 AA.
ID C7B1_THLAR
AC P49264.
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOCHROME P450 71B1 (EC 1.14.-.-) (CYPLXXIB1).
DE CYP71B1.
GN CYP71B1.
OS Thlaspi arvense (Field pennycress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eumids II; Brassicales; Brassicaceae; Thlaspi.
OX NCBI_TaxID=13288;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Shoot apex;
RX MEDLINE=94345014; PubMed=8066138;
RA Udvardi M.K., Metzger J.D., Krishnapillai V., Peacock W.J.,
RA Dennis E.S.;
RT "Cloning and sequencing of a full-length cDNA from Thlaspi arvense L.
RT that encodes a cytochrome P-450."
RL Plant Physiol. 105:755-756(1994).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
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CC -----
CC EMBL: L24438; AAA19701.1; .
CC DR InterPro: IPR001128; Cyt_P450.
CC DR Pfam: PF00067; p450; 1.
CC DR PRINTS: PR00463; EP4501.
CC DR PROSITE: PS00086; CYTOCHROME_P450; 1.
CC DR Oxidoreductase; Monooxygenase; Heme.
KW BINDING 436 436
FT BINDING 436 436 HEME (BY SIMILARITY).
SQ SEQUENCE 496 AA; 56387 MW; 59D3A6B34F6685D8 CRC64;

Query Match 50.0%; Score 42; DB 1; Length 496;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 RLMKKFKAEIRD 15
| | | | | | | |
Db 318 RVMKKLQAEIRE 329

RESULT 6
C726_ARATH STANDARD; PRT; 503 AA.
ID C726_ARATH
AC O65787;
```

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DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
OC CYTOCHROME P450 71B6 (EC 1.14.-.-).
GN CYP71B6 OR AT2G24180 OR F27D4.9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA; TISSUE=Seedling;
RA MEDLINE=96281573; PubMed=9620263;
RA Mizutani M., Ward E., Ohta D.;
RA "Cytochrome P450 superfamily in Arabidopsis thaliana: isolation of
RT cDNAs, differential expression, and RFLP mapping of multiple
RT cytochromes P450.";
RT Plant Mol. Biol. 37:39-52(1998).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA;
RC MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RA "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RT Nature 402:761-768(1999).
RL
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC
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CC -----
CC EMBL; D78604; BAA28536.1; .
CC DR EMBL; AC005967; AAD03379.1; .
CC DR InterPro; IPR001128; Cyt_P450.
CC DR Pfam; PF00067; p450; 1.
CC DR PRINTS; PS00463; EP4501.
CC DR PROSITE; PS00086; CYTOCHROME_P450; 1.
CC KW Oxidoreductase; Monooxygenase; Transmembrane; Heme; Multigene family.
FT TRANSMEM 10 30 POTENTIAL.
FT BINDING 446 446 HEME (BY SIMILARITY).
FT SEQUENCE 503 AA; 57008 MW; 71AFAD5370AEDFF6 CRC64;
SQ
Query Match 48.8%; Score 41; DB 1; Length 503;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 RLWKKFAEIRD 15
DB 328 RVKKVQAEIRE 339

RESULT 7
ID SYT_ARCFU STANDARD; PRT; 619 AA.
AC O29703;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE THREONYL-TRNA SYNTHETASE (EC 6.1.1.3) (THREONINE--TRNA LIGASE)

DE
Query Match 48.8%; Score 41; DB 1; Length 619;
Best Local Similarity 46.7%; Pred. No. 22;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATRLMKFKAEIRD 16
DB 88 AVKLLKQLEAEISDF 102

RESULT 8
ID RPCL_TRYBB STANDARD; PRT; 1530 AA.
AC P08958;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT (EC 2.7.7.6).
```



```
OS Trypanosoma brucei brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=427 / ISOLATE MITAT 1.2A;
RX MEDLINE=89016560; PubMed=3174432;
RA Cornelissen A.W.C.A., Evers R., Koeck J.;
RT "Structure and sequence of the gene for the largest subunit of
RL trypanosomal RNA polymerase III.";
RL Nucleic Acids Res. 16:8753-8772(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90036885; PubMed=2808366;
RA Smith J.L., Levin J.R., Agabian N.;
RT "Molecular characterization of the Trypanosoma brucei RNA polymerase
RL I and III largest subunit genes.";
RL J. Biol. Chem. 264:18091-18093(1989).
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +
CC RNA(N).
CC -!- SUBUNIT: RNA POLYMERASE III CONSISTS OF ABOUT 15 DIFFERENT
CC SUBUNITS. THIS SUBUNIT IS THE LARGEST COMPONENT OF RNA POLYMERASE
CC III.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE
CC FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
CC PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
CC III FOR 5S AND TRNA GENES.
CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
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CC -----
EMBL; X12494; CAA31014.1; -.
DR EMBL; M27163; AAA30233.1; -.
DR PIR; S01393; S01393.
DR InterPro; IPR000722; RNA_pol_A.
DR InterPro; IPR002879; RNA_pol_A2.
DR Pfam; PF00623; RNA_pol_A; 1.
DR Pfam; PF01854; RNA_pol_A2; 1.
DR Transferase; DNA-directed RNA polymerase; Transcription; Zinc;
KW zinc-finger; Nuclear protein.
FT ZN.FING 74 87
FT CONFLICT 1325 1325 D -> E (IN REF. 2).
FT CONFLICT 1493 1493 I -> V (IN REF. 2).
SQ SEQUENCE 1530 AA; 170271 MW; FC03D700CEFD742 CRC64;

Query Match 48.8%; Score 41; DB 1; Length 1530;
Best Local Similarity 63.6%; Pred. No. 57;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 KFKAEIRDF 17
Db 1035 RKFKDDIQDF 1045

RESULT 9
ID YMP9_CAEBL STANDARD; PRT; 194 AA.
AC Q10952;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 22.0 KDA PROTEIN B0361.9 IN CHROMOSOME III PRECURSOR.

GN B0361.9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2.
RA Du Z.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90036885; PubMed=2808366;
RA Smith J.L., Levin J.R., Agabian N.;
RT "Molecular characterization of the Trypanosoma brucei RNA polymerase
RL I and III largest subunit genes.";
RL J. Biol. Chem. 264:18091-18093(1989).
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +
CC RNA(N).
CC -!- SUBUNIT: RNA POLYMERASE III CONSISTS OF ABOUT 15 DIFFERENT
CC SUBUNITS. THIS SUBUNIT IS THE LARGEST COMPONENT OF RNA POLYMERASE
CC III.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE
CC FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
CC PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
CC III FOR 5S AND TRNA GENES.
CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC -----
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CC -----
EMBL; U00031; AAK18868.1; -.
DR WormPep; B0361.9; CE00838.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR Pfam; PF00024; PAN; 1.
DR SMART; SM00473; PAN_AP; 1.
DR Hypothetical protein; Signal.
KW SIGNAL 1 15
FT CHAIN 16 194
FT SIGNAL 1 15
FT SIGNAL 16 194 HYPOTHETICAL PROTEIN B0361.9.
SQ SEQUENCE 194 AA; 22017 MW; 79C9F7A2570AAAF38 CRC64;

Query Match 47.6%; Score 40; DB 1; Length 194;
Best Local Similarity 42.9%; Pred. No. 10;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 3 TRLMKFKAEIRDF 16
Db 170 SKLMKRLSAKREF 183

RESULT 10
C72Q_ARATH
ID C72Q_ARATH STANDARD; PRT; 500 AA.
AC Q9LTL0;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CYTOCHROME P450 71B26 (EC 1.14.-.-).
GN CYP71B26 OR AT3G26290 OR MTC11.22.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta;
OC Arabidopsida; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20277480; PubMed=10819329;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
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CC -----
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DR EMBL; AB024038; BAB02452.1; -.
DR InterPro: IPR001128; Cyt_P450.
DR Pfam: PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Transmembrane; Heme; Multigene family.
FT TRANSMEM 1 21 POTENTIAL.
FT BINDING 440 440 HEME (BY SIMILARITY).
SQ SEQUENCE 500 AA; 57080 MW; 7BD8352058P4C52C CRC64;

Query Match 47.6%; Score 40; DB 1; Length 500;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 RLMKKFAEIRD 15
      : : : : :
Db 322 RVMKVQAEIRN 333

RESULT 11
C7C3_MAIZE STANDARD; PRT; 535 AA.
AC P93703; Q43256;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE CYTOCHROME P450 71C3 (EC 1.14.-.-).
GN CYP71C3.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE OF 535 FROM N.A.
RC STRAIN=CV. CI31A;
RA Frey M., Kliehm R., Siedler H., Gierl A.;
RT "Expression of a cytochrome P450 gene family in maize.";
RL Mol. Gen. Genet. 246:100-109(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. CI31A;
RA Gierl A.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X81830; CAA57424.2; ALT_SEQ.
DR EMBL; Y11403; CAA72207.1; -.
DR InterPro: IPR001128; Cyt_P450.
DR Pfam: PF00067; P450; 1.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Transmembrane; Heme.
FT TRANSMEM 23 43 POTENTIAL.
FT BINDING 475 475 HEME (BY SIMILARITY).
SQ SEQUENCE 535 AA; 60715 MW; F92A696108E2ADAF CRC64;

Query Match 47.6%; Score 40; DB 1; Length 535;
Best Local Similarity 53.8%; Pred. No. 28;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 RLMKKFAEIRD 16
      : : : : :
Db 322 RVMKVQAEIRN 333
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Db 351 RVMKLQAEVRAY 363

RESULT 12
VP4_ROTHT STANDARD; PRT; 774 AA.
ID VP4_ROTHT
AC P11200;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4)
DE [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8].
GN S4.
OS Human rotavirus (serotype 4 / strain St. Thomas 3).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=10960;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=88275070; PubMed=2839714;
RA Gorziglia M., Green K., Nishikawa K., Taniguchi K., Jones R.,
RA Kapikian A.Z., Chanock R.M.;
RT "Sequence of the fourth gene of human rotaviruses recovered from
RT asymptomatic or symptomatic infections.";
RL J. Virol. 62:2978-2984(1988).
RN [2]
RP SEQUENCE OF 1-280.
RX MEDLINE=86313706; PubMed=3018754;
RA Gorziglia M., Hoshino Y., Buckler-White A., Blumentals I., Glass R.,
RA Flores J., Kapikian A.Z., Chanock R.M.;
RT "Conservation of amino acid sequence of VP8 and cleavage region of
RT 84-kDa outer capsid protein among rotaviruses recovered from
RT asymptomatic neonatal infection.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:7039-7043(1986).
CC -1- SUBCELLULAR LOCATION: OUTER CAPSID.
CC -1- PTM: VP8 IS ONE OF TWO TRYPSIN CLEAVAGE PRODUCTS OF VP4; THE
CC OTHER PRODUCT IS VP5.
CC -1- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
DR PIR; H28839; VEXRWT.
DR InterPro: IPR000416; Cap_VP4.
DR Pfam: PF00426; VP4; 1.
KW Coat protein; Glycoprotein.
FT CHAIN 1 774 OUTER CAPSID PROTEIN VP4.
FT CHAIN 247 774 OUTER CAPSID PROTEIN VP5.
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 583 583 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 774 AA; 87455 MW; D397E5C6125A8FA8 CRC64;

Query Match 47.6%; Score 40; DB 1; Length 774;
Best Local Similarity 70.0%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LATRLMKKFK 10
      : : : : :
Db 543 MATKVMKKFK 552

RESULT 13
VP4_ROTHT STANDARD; PRT; 775 AA.
ID VP4_ROTHT
AC P11197;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
```

20-AUG-2001 (Rel. 40, Last annotation update)  
DE OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4)  
DE [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8].

S4.  
GN Human rotavirus (serotype 1 / strain M37).

OC Viruses: dsRNA viruses; Reoviridae; Rotavirus.

ON NCBI\_TaxID=10954;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88275070; PubMed=2839714;

RA Gorziglia M., Green K., Nishikawa K., Taniguchi K., Jones R.,

RA Kapikian A.Z., Chanock R.M.;

RT "Sequence of the fourth gene of human rotaviruses recovered from

RT asymptomatic or symptomatic infections.";

RL J. Virol. 62:2978-2984(1988).

RN [2]

RP SEQUENCE OF 1-280.

RX MEDLINE=86313706; PubMed=3018754;

RA Gorziglia M., Hoshino Y., Buckler-White A., Blumentals I., Glass R.,

RA Flores J., Kapikian A.Z., Chanock R.M.;

RT "Conservation of amino acid sequence of VP8 and cleavage region of

RT 84-kDa outer capsid protein among rotaviruses recovered from

RT asymptomatic neonatal infection.";

RL Proc. Natl. Acad. Sci. U.S.A. 83:7039-7043(1986).

CC -1- SUBCELLULAR LOCATION: OUTER CAPSID.

CC -1- PTM: VP8 IS ONE OF TWO TRYPSIN CLEAVAGE PRODUCTS OF VP4; THE

CC OTHER PRODUCT IS VP5.

CC -1- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.

DR PIR: E28839; VPRW7.

DR InterPro: IPR000416; Cap\_VP4.

DR Pfam: PF00426; VP4; 1.

KW Coat protein; Glycoprotein.

FT CHAIN 1 775

FT CHAIN 1 775

FT CARBOHYD 32 32

FT CARBOHYD 56 56

FT CARBOHYD 97 97

FT CARBOHYD 111 111

FT CARBOHYD 114 114

FT CARBOHYD 132 132

FT CARBOHYD 146 146

FT CARBOHYD 192 192

FT CARBOHYD 277 277

FT CARBOHYD 324 324

FT CARBOHYD 583 583

FT CARBOHYD 606 606

FT CARBOHYD 775 AA; 87402 MW; 05CA6DDAA258550B CRC64;

SQ SEQUENCE 775 AA; 87402 MW; 05CA6DDAA258550B CRC64;

Query Match 47.6%; Score 40; DB 1; Length 775;

Best Local Similarity 70.0%; Pred. No. 42;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LATRLMKKFK 10

Db 543 MATKVMKKFK 552

RESULT 14

VP4\_ROTIN

ID VP4\_ROTIN STANDARD; PRT; 776 AA.

AC P11199;

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4)

DE [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8].

S4.

GN Human rotavirus (serotype 3 / strain McN13).

OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.

ON NCBI\_TaxID=10955;

RN [1]

SEQUENCE FROM N.A.

RX MEDLINE=88275070; PubMed=2839714;

RA Gorziglia M., Green K., Nishikawa K., Taniguchi K., Jones R.,

RA Kapikian A.Z., Chanock R.M.;

RT "Sequence of the fourth gene of human rotaviruses recovered from

RT asymptomatic or symptomatic infections.";

RL J. Virol. 62:2978-2984(1988).

RN [2]

RP SEQUENCE OF 1-281.

RX MEDLINE=86313706; PubMed=3018754;

RA Gorziglia M., Hoshino Y., Buckler-White A., Blumentals I., Glass R.,

RA Flores J., Kapikian A.Z., Chanock R.M.;

RT "Conservation of amino acid sequence of VP8 and cleavage region of

RT 84-kDa outer capsid protein among rotaviruses recovered from

RT asymptomatic neonatal infection.";

RL Proc. Natl. Acad. Sci. U.S.A. 83:7039-7043(1986).

CC -1- SUBCELLULAR LOCATION: OUTER CAPSID.

CC -1- PTM: VP8 IS ONE OF TWO TRYPSIN CLEAVAGE PRODUCTS OF VP4; THE

CC OTHER PRODUCT IS VP5.

CC -1- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.

DR PIR: G28839; VPRW9.

DR InterPro: IPR000416; Cap\_VP4.

DR Pfam: PF00426; VP4; 1.

KW Coat protein; Glycoprotein.

FT CHAIN 1 776

FT CHAIN 1 776

FT CARBOHYD 32 32

FT CARBOHYD 56 56

FT CARBOHYD 97 97

FT CARBOHYD 111 111

FT CARBOHYD 114 114

FT CARBOHYD 132 132

FT CARBOHYD 193 193

FT CARBOHYD 278 278

FT CARBOHYD 325 325

FT CARBOHYD 584 584

FT CARBOHYD 607 607

FT CONFLICT 190 190

FT MISSING (IN REF. 2).

SQ SEQUENCE 776 AA; 87794 MW; CFCADF4DEE986512 CRC64;

Query Match 47.6%; Score 40; DB 1; Length 776;

Best Local Similarity 70.0%; Pred. No. 42;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LATRLMKKFK 10

Db 544 MATKVMKKFK 553

RESULT 15

LGT\_RICPR

ID LGT\_RICPR STANDARD; PRT; 268 AA.

AC Q9ZE99;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE PROLIPOPROTEIN DIACYLGLYCERYL TRANSFERASE (EC 2.4.99.-).

GN LGT OR RP046.

OS Rickettsia prowazekii.

OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;

OC Rickettsiaceae; Rickettsia;

ON NCBI\_TaxID=782;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99039499; PubMed=9823893;

RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,

RA Sichertitz-Ponten T., Alsmark U.C.M., Podowski R.M.,

RA Eriksson A.-S., Winkler H.H., Kurland C.G.;

RT "The genome sequence of Rickettsia prowazekii and the origin of

```

RT mitochondria."
RL Nature 396:133-140(1998).
CC -1- FUNCTION: TRANSFERS THE N-ACYL DIGLYCERIDE GROUP ON WHAT WILL
CC BECOME THE N-TERMINAL CYSTEINE OF MEMBRANE LIPOPROTEINS
CC (BY SIMILARITY).
CC -1- PATHWAY: FIRST STEP IN LIPOPROTEIN BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE LGT FAMILY.
CC -----
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CC -----
CC EMBL; AJ235270; CAA14517.1; -.
CC InterPro; IPR001640; LGT.
CC Pfam; PF01790; LGT; 1.
CC PROSITE; PS01311; LGT; 1.
CC Transferase; Transmembrane; Complete proteome.
FT TRANSMEM 18 38 POTENTIAL.
FT TRANSMEM 64 84 POTENTIAL.
FT TRANSMEM 101 121 POTENTIAL.
FT TRANSMEM 126 146 POTENTIAL.
FT TRANSMEM 181 201 POTENTIAL.
FT TRANSMEM 210 230 POTENTIAL.
FT TRANSMEM 237 257 POTENTIAL.
SQ SEQUENCE 268 AA; 30556 MW; 451588ABF12F58A3 CRC64;

```

Query Match 46.4%; Score 39; DB 1; Length 268;  
Best Local Similarity 58.3%; Pred. No. 20;  
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATRLMKKFKAEI 13.  
|:::| |  
Db 45 ATKIERFKPEI 56

Search completed: January 29, 2002, 11:16:19  
Job time: 148 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 11:15:52 ; Search time 62.77 Seconds  
(without alignments)  
39.615 Million cell updates/sec

Title: US-09-763-397A-23

Perfect score: 84

Sequence: 1 LATRLMKKFAEIRDF 17

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_17:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organalle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	84	100.0	153	5 Q25763	Q25763 plasmodium
2	84	100.0	161	5 Q25764	Q25764 plasmodium
3	84	100.0	163	5 Q27330	Q27330 plasmodium
4	84	100.0	782	5 Q25730	Q25730 plasmodium
5	84	100.0	782	5 Q25875	Q25875 plasmodium
6	84	100.0	782	5 Q26007	Q26007 plasmodium
7	84	100.0	782	5 Q9U431	Q9U431 plasmodium
8	84	100.0	782	5 Q9U430	Q9U430 plasmodium
9	84	100.0	782	5 Q9U429	Q9U429 plasmodium
10	84	100.0	782	5 Q9U414	Q9U414 plasmodium
11	81	96.4	782	5 Q26104	Q26104 plasmodium
12	44	52.4	1089	10 Q9LUS2	Q9LUS2 arabidopsis
13	43	51.2	353	10 Q9SB32	Q9SB32 arabidopsis
14	43	51.2	649	5 Q9VEU6	Q9VEU6 drosophila
15	42	50.0	398	10 Q9XEC5	Q9XEC5 arabidopsis
16	42	50.0	456	1 Q58576	Q58576 pyrococcus
17	42	50.0	534	12 Q65856	Q65856 beet yellow
18	42	50.0	743	10 Q9ZWA0	Q9ZWA0 arabidopsis
19	42	50.0	797	5 Q9NKN3	Q9NKN3 leishmania

#### ALIGNMENTS

RESULT 1

Q25763 ID Q25763 PRELIMINARY; PRT; 153 AA.  
AC Q25763;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel.. 01, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE STRAIN INDJ-1 RHOPTRY-ASSOCIATED PROTEIN 1 (RAP-1) (FRAGMENT).  
GN RAP-1.  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-INDJ-1 (CLONE 1 OF INDIAN ISOLATE J);  
RX MEDLINE=92244303; PubMed=1574089;  
RA Howard R.F.; Peterson C.;  
RT "The sequence of the p82 rhoptry protein is highly conserved between two Plasmodium falciparum isolates.";  
RL Mol. Biochem. Parasitol. 51:327-330(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-INDJ-1 (CLONE 1 OF INDIAN ISOLATE J);  
RX MEDLINE=96379224; PubMed=8784775;  
RA Howard R.F.; Peterson C.;  
RT "Limited RAP-1 sequence diversity in field isolates of Plasmodium falciparum";  
RL Mol. Biochem. Parasitol. 77:95-98(1996).  
DR EMBL; U41075; AAC47091.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 153 153  
SQ SEQUENCE 153 AA; 18273 MW; 6AA7AC3C4AAC447C CRC64;

Query Match 100.0%; Score 84; DB 5; Length 153;  
Best Local Similarity 100.0%; Pred. No. 4.1e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LATRLMKKFAEIRDF 17

|||||

119 LATRLMKKFAEIRDF 135

DB

Q9zvJ6 arabidopsis  
Q08367 zea mays (m  
Q43248 zea mays (m  
Q41743 zea mays (m  
O71199 plasmodium  
Q9b4t5 homo sapien  
Q91402 pseudomonas  
Q99j12 mus musculu  
Q9shg1 arabidopsis  
Q9sb33 arabidopsis  
Q9sup2 arabidopsis  
Q93989 bacteriophag  
O76308 trichomonas  
Q00827 trichomonas  
Q99ty3 tetrahymena  
O61712 caenorhabdi  
Q9n4k2 caenorhabdi  
Q86201 human rotav  
Q86221 rotavirus s  
Q86223 rotavirus s  
Q82119 human rotav  
Q90314 human rotav  
Q90315 human rotav  
Q9s1f3 arabidopsis  
Q9zhf5 streptococc  
Q9zu08 arabidopsis

RESULT 2  
Q25764 PRELIMINARY; PRT; 161 AA.  
AC Q25764;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE STRAIN INDJ-2 RHOPTRY-ASSOCIATED PROTEIN 1 (RAP-1) (FRAGMENT).  
GN RAP-1.  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-INDJ-2 (CLONE 2 OF INDIAN ISOLATE J);  
RX MEDLINE=92244303; PubMed=1574089;  
RA Howard R.F.;  
RT "The sequence of the p82 rhopty protein is highly conserved between two Plasmodium falciparum isolates."  
RL Mol. Biochem. Parasitol. 51:327-330(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-INDJ-2 (CLONE 2 OF INDIAN ISOLATE J);  
RX MEDLINE=96379224; PubMed=8784775;  
RA Howard R.F., Peterson C.;  
RT "Limited RAP-1 sequence diversity in field isolates of Plasmodium falciparum."  
RL Mol. Biochem. Parasitol. 77:95-98(1996).  
DR EMBL; U41076; AAC47092.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 161 161  
SQ SEQUENCE 161 AA; 19271 MW; 2433BF4A2FEE2F72 CRC64;

Query Match 100.0%; Score 84; DB 5; Length 161;  
Best Local Similarity 100.0%; Pred. No. 4.4e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LATRLMKKFKAEIRDFF 17  
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Db 122 LATRLMKKFKAEIRDFF 138

RESULT 3  
Q27330 PRELIMINARY; PRT; 163 AA.  
AC Q27330;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE STRAIN INDJ-2 RHOPTRY-ASSOCIATED PROTEIN 1 (RAP-1) (FRAGMENT).  
GN RAP-1.  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-INDC (INDIAN ISOLATE C);  
RX MEDLINE=92244303; PubMed=1574089;  
RA Howard R.F.;  
RT "The sequence of the p82 rhopty protein is highly conserved between two Plasmodium falciparum isolates."  
RL Mol. Biochem. Parasitol. 51:327-330(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-INDC (INDIAN ISOLATE C);  
RX MEDLINE=96379224; PubMed=8784775;  
RA Howard R.F., Peterson C.;  
RT "Limited RAP-1 sequence diversity in field isolates of Plasmodium falciparum."  
RL Mol. Biochem. Parasitol. 77:95-98(1996).  
DR EMBL; U41077; AAC47093.1; -.

DR EMBL; U41073; AAC47089.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 163 163  
SQ SEQUENCE 163 AA; 19522 MW; BD43E37992DF3730 CRC64;  
  
Query Match 100.0%; Score 84; DB 5; Length 163;  
Best Local Similarity 100.0%; Pred. No. 4.4e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 LATRLMKKFKAEIRDFF 17  
|||||  
Db 124 LATRLMKKFKAEIRDFF 140  
  
RESULT 4  
Q25730 PRELIMINARY; PRT; 782 AA.  
AC Q25730;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE RHOPTRY ASSOCIATED PROTEIN-1.  
GN RAP-1.  
OS Plasmodium falciparum (isolate FC27 / Papua New Guinea).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5837;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FC27;  
RA Shi Y., Lai A.A.;  
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U20985; AAA63681.1; -.  
SQ SEQUENCE 782 AA; 90023 MW; F69E26A2A564C8EA CRC64;

Query Match 100.0%; Score 84; DB 5; Length 782;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LATRLMKKFKAEIRDFF 17  
|||||  
Db 736 LATRLMKKFKAEIRDFF 752

RESULT 5  
Q25875 PRELIMINARY; PRT; 782 AA.  
AC Q25875;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE PR86 RHOPTRY PRECURSOR PROTEIN.  
GN P82.  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HONDURAS I CDC;  
RX MEDLINE=90348711; PubMed=2200961;  
RA Ridley R.G., Takacs B., Lahm H.W., Delves C.J., Goman M., Certa V.,  
Matile H., Woollett G.R., Scaife J.G.;  
RT "Characterisation and sequence of a protective rhopty antigen from Plasmodium falciparum."  
RL Mol. Biochem. Parasitol. 41:125-134(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HONDURAS I CDC;  
RX MEDLINE=92244303; PubMed=1574089;  
RA Howard R.F.;  
RT "The sequence of the p82 rhopty protein is highly conserved between two Plasmodium falciparum isolates."  
DR EMBL; U41077; AAC47093.1; -.



Mon Feb 4 15:23:45 2002

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RESULT 10
Q9U414 ID Q9U414 PRELIMINARY; PRT; 782 AA.
AC Q9U414;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE RHOPTRY ASSOCIATED PROTEIN-1.
GN RAP-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FCCL/HN;
RA Li X.R., Luo S.H., Yu X.B., Shan Z.X., Ma C.L.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF206631; AAF15365.1; -.
SQ SEQUENCE 782 AA; 90082 MW; 8E1F4CF2883903FD CRC64;

Query Match 100.0%; Score 84; DB 5; Length 782;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LATRLMKKFKAEIRDF 17
Db 736 LATRLMKKFKAEIRDF 752

RESULT 11
Q26104 ID Q26104 PRELIMINARY; PRT; 782 AA.
AC Q26104;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE RHOPTRY ASSOCIATED PROTEIN 1.
GN RAP-1.
OS Plasmodium reichenowi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5854;
RN [1]
RP SEQUENCE FROM N.A.
RA Shi Y., Lai A.A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U20986; AAA63682.1; -.
SQ SEQUENCE 782 AA; 90160 MW; DE6D1BE2FAC308A9 CRC64;

Query Match 96.4%; Score 81; DB 5; Length 782;
Best Local Similarity 94.1%; Pred. No. 6.6e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LATRLMKKFKAEIRDF 17
Db 736 LATRLMKKFKAEIRDF 752

RESULT 12
Q9LU52 ID Q9LU52 PRELIMINARY; PRT; 1089 AA.
AC Q9LU52;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CHLOROPLAST OUTER ENVELOPE PROTEIN-LIKE.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
```

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RN SEQUENCE FROM N.A.
RP STRAIN=COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
DR EMBL: AB022217; BAB02753.1; -.
KW Envelope protein.
SQ SEQUENCE 1089 AA; 119917 MW; 2ED2EAB60E409C7E CRC64;

Query Match 52.4%; Score 44; DB 10; Length 1089;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 RLMKKFKAEIRD 15
Db 784 KLLKKFAEIKD 795

RESULT 13
Q9SB32 ID Q9SB32 PRELIMINARY; PRT; 353 AA.
AC Q9SB32;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE SRG1-LIKE PROTEIN.
GN P24A6.150 OR AT4G25310.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Wedler H., Wambutt R., Hoheisel J., Mewes H.W.,
RA Mayer K.F.X., Schaefer C.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Wedler H., Wedler E., Wambutt R., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 216-353 FROM N.A.
RA Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL035396; CAA23072.1; -.
DR EMBL: AL161563; CAB81342.1; -.
DR InterPro; IPR002419; Fe_asc_oxidore.
DR InterPro; IPR002283; IPN_Synth.
DR Pfam; PF00671; Fe_Asc_Oxidore; 1.
DR PRINTS; PR00682; IPNSYNTHASE.
SQ SEQUENCE 353 AA; 39933 MW; 5D61270C34721034 CRC64;

Query Match 51.2%; Score 43; DB 10; Length 353;
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Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 MKKFAEIRDF 17
Db 92 LDKSKSDIOFF 103
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RESULT 14
Q9VEU6 PRELIMINARY; PRT; 649 AA.
AC Q9VEU6;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE CG14885 PROTEIN.
GN CG14885.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Morkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AF003713; AAF55322.1; -.
DR HSP: P16068; IAWN.
DR FlyBase: FBgn0038435; CG14885.
DR InterPro: IPR001054; Guanylt_cyclase.
DR Pfam: PF00211; guanylate_cyc; 1.
DR SMART: SM00044; CYCC; 1.
DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.
DR PROSITE: PS0125; GUANYLATE_CYCLASES_2; 1.
KW Lyase.
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Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LATRLMKKFKKA 11
Db 546 LALRVNKKFKA 556
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RESULT 15
Q9XEC5 PRELIMINARY; PRT; 398 AA.
AC Q9XEC5;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE HYPOTHETICAL 44.0 KDA PROTEIN.
GN T26N6.8 OR AT4G04480.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Zhong J., Ma P., Parnell L.D., Chen C.-N., Chen E.Y.;
RT "Genomic sequence of Arabidopsis thaliana BAC T26N6, chromosome IV,
RT 19.3 cm.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Zhong J., Ma P., Parnell L.D., Chen C.N., Chen E.Y.; Mewes H.W.,
RA Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF076243; AAD29760.1; -.
DR EMBL: AL161500; CAB77916.1; -.
KW Hypothetical protein.
SQ SEQUENCE 398 AA; 43961 MW; 0077BE2298E94AD7 CRC64;

Query Match 50.0%; Score 42; DB 10; Length 398;
Best Local Similarity 60.0%; Pred. No. 70;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATRLMKKFAEIRDF 16
Db 165 ATRLFKKLRVEIMF 179
: |||:|:|

Search completed: January 29, 2002, 11:15:52
Job time: 212 sec
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run On: January 29, 2002, 10:59:19 ; Search time 66.28 Seconds  
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16.764 Million cell updates/sec

Title: US-09-763-397A-24

Perfect score: 74

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Scoring table: BLOSUM62

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Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	74	100.0	15	11	AA06310		Tetanus toxin epit
2	74	100.0	15	18	AAW35506		Universal T-cell e
3	74	100.0	15	18	AAW11505		Tetanus toxoid uni
4	74	100.0	15	19	AAW67033		Tetanus toxin frag
5	74	100.0	15	19	AAW71321		Universal helper T
6	74	100.0	15	20	AAW04051		T-Helper epitope f
7	74	100.0	15	20	AAW67578		T-cell epitope pep
8	74	100.0	15	20	AAW73220		Tetanus toxoid epi
9	74	100.0	15	21	AAW45511		Tetanus P2 epitope
10	74	100.0	15	21	AAW82637		Tetanus toxoid T c
11	74	100.0	15	21	AAW92625		Foreign epitope P2

12	74	100.0	15	21	AAW84427	Amino acid sequenc
13	74	100.0	15	21	AAW70300	Clostridium tetani
14	74	100.0	15	21	AAW44763	Tetanus toxoid pro
15	74	100.0	15	22	AAW85451	Wild-type TT830 (t
16	74	100.0	15	22	AAW61956	Tetanus toxoid uni
17	74	100.0	15	22	AAW20143	Tetanus toxin T-ce
18	74	100.0	15	22	AAW68636	HER-2 B cell pepti
19	74	100.0	15	22	AAW46172	Tetanus toxoid TT8
20	74	100.0	15	22	AAW49071	Tetanus toxoid TT
21	74	100.0	16	18	AAW35445	T-cell stimulatory
22	74	100.0	16	20	AAW23705	Clostridium tetani
23	74	100.0	17	15	AAW62692	Helper T cell epit
24	74	100.0	17	16	AAW82573	Tetanus toxin help
25	74	100.0	17	17	AAW05599	Tetanus toxin help
26	74	100.0	17	17	AAW88395	T-cell antigen TT2
27	74	100.0	17	21	AAW99274	HLA class II bindi
28	74	100.0	17	21	AAW80056	Pathogen derived T
29	74	100.0	17	21	AAW54539	T helper cell (Th)
30	74	100.0	17	21	AAW58768	Unidentified pepti
31	74	100.0	17	22	AAW62904	Amino acid residue
32	74	100.0	17	22	AAW84435	Amino acid sequenc
33	74	100.0	17	22	AAW30941	Antigenic fragment
34	74	100.0	17	22	AAW31029	Antigenic fragment
35	74	100.0	17	22	AAW31118	Antigenic fragment
36	74	100.0	17	22	AAW15589	Peptide 5 for pept
37	74	100.0	18	20	AAW26607	HIV-derived lipope
38	74	100.0	19	21	AAW99055	HLA class II bindi
39	74	100.0	22	22	AAW46175	Tetanus toxoid 830
40	74	100.0	22	22	AAW46178	Tetanus toxoid 830
41	74	100.0	22	22	AAW46196	Tetanus toxoid epi
42	74	100.0	22	22	AAW46203	Human APP A-beta 1
43	74	100.0	25	21	AAW92650	PSMpep007 - P2 ins
44	74	100.0	25	21	AAW92651	PSMpep008 - P2 ins
45	74	100.0	25	21	AAW92652	PSMpep009 - P2 ins

#### ALIGNMENTS

RESULT 1  
AA06310  
ID AA06310 standard; protein; 15 AA.  
XX  
AC AA06310;  
XX  
DT 04-DEC-1990 (first entry)  
XX  
DE Tetanus toxin epitope.  
XX  
KW Tetanus toxin; vaccine; major histocompatibility complex; MHC;  
KW antimalarial.  
XX  
OS Synthetic.  
XX  
PN Ep378881-A.  
XX  
PD 25-JUL-1990.  
XX  
PF 27-DEC-1989; 89EP-0203318.  
XX  
PR 16-NOV-1989; 89IT-0022409.  
PR 17-JAN-1989; 89IT-0019110.  
XX  
PA (ENTE ) ENRERICHE SPA.  
XX  
PI Pessi A, Bianchi E, Verdini AS, Corradin G;  
XX  
DR WPI; 1990-225582/30.  
XX  
PT Synthetic peptide(s) corresp. to tetanus toxin epitope(s) - used  
PT as universal carriers for prepn. of immunogenic conjugate(s) for  
PT use as vaccines.  
XX

PS Claim 1; Page 17; 20pp; English.

XX Epitopic peptides may be used with synthetic hapten derived from  
 CC a pathogen to generate an immune response to the pathogen.  
 CC Peptides are recognised by numerous T-helper cell clones within  
 CC the context of a wide range of alleles of the human MHC.  
 CC The peptides may be used in an antimalarial vaccine inducing Ab.  
 CC response to P.falciparum.  
 XX  
 SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 11; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15  
 DB 1 qyikanskfigitel 15  
 |||||

RESULT 2  
 AAW35506  
 ID AAW35506 standard; peptide; 15 AA.  
 XX  
 AC AAW35506;

DT 22-APR-1998 (first entry)

DE Universal T-cell epitope peptide SEQ ID NO:8.

KW T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;  
 KW scaffold; inhibition; metastasis; wound healing; solid phase.  
 XX

OS Unidentified.

PN WO9738011-A1.

PD 16-OCT-1997.

PF 03-APR-1997; 97WO-DE00146.

PR 03-APR-1996; 96DK-0000398.

PA (PEPR-) PEPRESEARCH AS.

PI Heegaard PMH, Jakobsen PH;

DR WPI; 1997-512645/47.

XX Non-dendritic peptide carrier linked to a solid phase - useful as a  
 PT diagnostic agent and as a scaffold for production of chemical  
 PT derivatives

PS Example 20; Page 124; 262pp; English.

XX A non-dendritic peptide carrier (A) has been developed which is coupled  
 CC through a linker to a solid phase, forming a complex of (A)-solid phase.  
 CC where (A) comprises 10-50 amino acids capable of forming a secondary  
 CC structure in a benign buffer after liberation from the solid phase, and  
 CC further the (A)-solid phase complex comprises an immunogenic substance  
 CC and/or an immune mediator coupled on (A). The present sequence  
 CC represents a peptide used in an example from the present invention. An  
 CC (A)-solid phase complex can be used as a scaffold for the production of  
 CC chemical derivatives, characterised by covalently attaching molecules at  
 CC attachment points. Alternatively (A) is used as a scaffold-peptide for  
 CC the incorporation into an Immunostimulating Complex (Iscom) resulting an  
 CC (A)-Iscom complex which is used for the chemical coupling of antigenic  
 CC substances in an aqueous solution by conjugation. (A) derivatised with  
 CC one or more peptides having fibronectin-, laminin- or vitronectin-like  
 CC binding activities can be used for the promotion of cell-attachment to  
 CC plastic surfaces, in particular to inhibit tumour growth and metastasis,  
 CC and for promotion of wound healing. Also a derivatised (A) can be used

CC for the selection of specifically-binding aptamers or as a diagnostic  
 CC agent. Such diagnostic-(A) molecules could be used to detect molecules  
 CC derived from or indicative of pregnancy or of a disease, such as an  
 CC infectious, autoimmune or cancerous disease.  
 XX  
 SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15  
 DB 1 qyikanskfigitel 15  
 |||||

RESULT 3  
 AAW11505  
 ID AAW11505 standard; Protein; 15 AA.  
 XX  
 AC AAW11505;

DT 24-SEP-1997 (first entry)

DE Tetanus toxoid universal Th epitope TT830.

KW Humanised antibody; anti-Fc receptor; H22; bifunctional; bispecific;  
 KW fusion protein; chimera; tetanus toxoid; helper T cell epitope;  
 KW antigen presentation; ds.  
 XX

OS Clostridium tetani.

PN WO9640789-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US09988.

PR 07-JUN-1995; 95US-0484172.

PA (MEDA-) MEDAREX INC.

PI Deo YM, Goldstein J, Graziano R, Somasundaram C;

DR WPI; 1997-052242/05.

DR N-PSDB; AAT58127.

XX Recombinant, multi-specific anti-Fc receptor antibody molecules -  
 PT also comprise an anti-target portion, used for the treatment of  
 PT cancer, autoimmune disease and pathogenic infection

PS Example 7; Fig 24; 115pp; English.

XX Synthetic DNA coding for the wild-type universal Th epitope from  
 CC tetanus toxoid, designated TT830, was fused to the 3'-end of DNA  
 CC encoding heavy chain sequences from the humanised anti-Fc gamma RI  
 CC monoclonal antibody H22. The resulting fusion protein was shown to  
 CC be significantly more efficient in antigen presentation and T cell  
 CC stimulation than the TT830 epitope alone. A similar fusion  
 CC construct was prepared coding for a mutant, antagonistic form of the  
 CC epitope (designated TT833S) fused to the anti-Fc gamma RI. The  
 CC Fab22-TT833S is at least 100 times more effective than TT833S in  
 CC inhibiting T cell activation.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15

```

Db      1 qiykanskfigitel 15
|||||
RESULT 4
AAW67033
ID AAW67033 standard; peptide; 15 AA.
XX
AC AAW67033;
XX
DT 15-DEC-1998 (first entry)
XX
DE Tetanus toxin fragment (residues 830-844).
XX
KW Tetanus toxin; vaccine; antibody; carbohydrate peptide conjugate;
KW dendrimeric poly-lysine; epitope; tumour.
XX
OS Clostridium tetani.
XX
PN WO9843677-A1.
XX
PD 08-OCT-1998.
XX
PF 27-MAR-1998; 98WO-EP01922.
XX
PR 27-MAR-1997; 97US-0041726.
XX
PA (INSP ) INST PASTEUR.
XX
PI Bay S, Cantacuzene D, Leclerc C, Lo-man R;
XX
DR WPI; 1998-557071/47.
XX
PT Carbohydrate peptide conjugate used as vaccine - comprises carrier
PT with dendrimeric poly-lysine enabling multiple epitopes to be
PT covalently attached
XX
PS Disclosure: Page 13; 55pp; English.
XX
CC The invention relates to a new carbohydrate peptide conjugate, which
CC comprises a carrier with a dendrimeric poly-lysine enabling multiple
CC epitopes to be covalently attached to it. Also claimed are: (1) an
CC antibody purified from biological fluid or cells of organisms
CC administered with the carbohydrate peptide conjugate, and (2) a diagnosis
CC kit comprising antigen-specific antibodies elicited by immunisation with
CC the carbohydrate peptide conjugate. The peptide conjugate, antibody and
CC diagnosis kit are used to provide pharmaceutical compositions and
CC vaccines against tumours. These can be used to support an immune response
CC against viral infections caused by hepatitis virus, HIV or cytomegalo
CC virus. They can be used to enhance immune responses, especially B- and T-
CC cell responses, of humans and animals against bacterial infections. The
CC carbohydrate peptide conjugate stimulates the antibody and T-cell
CC response without stimulating undesired immune responses. The composition
CC is capable of increasing the survival of tumour bearing humans and
CC animals. The present sequence corresponds to residues 830-844 of tetanus
CC toxin. The synthetic peptide corresponding to this sequence may be used
CC as an epitope in a carbohydrate peptide conjugate.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 19; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15
Db 1 qiykanskfigitel 15

RESULT 5
AAW71321
ID AAW71321 standard; peptide; 15 AA.
XX
AC AAW71321;
XX
DT 26-NOV-1998 (first entry)
XX
DE Universal helper T-cell epitope P2 derived from tetanus toxin.
XX
KW Liver stage; Plasmodium; Navy Yoelii Liver Stage 3 antibody; NYLS3;
KW hepatic and erythrocytic stage protein; PyHEP17; vaccine;
KW malaria parasite; teanus toxin; P2; helper T-cell epitope.
XX
OS Synthetic.
OS Clostridium tetani.
XX
PN US5814617-A.
XX
PD 29-SEP-1998.
XX
PF 07-OCT-1994; 94US-0319704.
XX
PR 07-OCT-1994; 94US-0319704.
XX
PA (USNA ) US SEC OF NAVY.
XX
PI Charoenvit Y, Doolan DL, Hedstrom RC, Hoffman SL;
XX
DR WPI; 1998-541794/46.
XX
PT Vaccine for protecting mammal against infection by malaria caused by
PT Plasmodium species - comprises a first nucleic acid encoding a first
PT polypeptide capable of eliciting an immune reaction against an
PT antigen expressed during the liver
XX
PS Disclosure; Column 12; 24pp; English.
XX
CC AAW71321-22 represent universal helper T-cell epitopes derived from
CC tetanus toxin. They are used to enhance host immune response to
CC vaccines. The specification describes a Plasmodium yoelii liver stage
CC 17 kDa hepatic and erythrocytic stage protein designated PyHEP17. This
CC protein elicits a response from an Igi monoclonal antibody designated
CC Navy Yoelii Liver Stage 3 (NYLS3). This antibody does not recognise
CC sporozoites, but does recognise P. yoelii liver stage parasites. NYLS3
CC eliminates upto 90% of liver stage parasites. The specification
CC describes a vaccine for reducing the severity or incidence of infection
CC by a malaria parasite of the genus Plasmodium. The DNA vaccine comprises
CC exon 1 and part of exon 2 of the PyHEP17 gene.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 19; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15
Db 1 qiykanskfigitel 15

RESULT 6
AAW04051
ID AAY04051 standard; peptide; 15 AA.
XX
AC AAY04051;
XX
DT 04-JAN-2000 (first entry)
XX
DE T-Helper epitope from tetanus toxoid.
XX
KW Covalently reactive antigen analog; CRAA; catalytic antibody;
KW electrophilic reaction centre; phosphonate; boronate; vaccine;
KW transition state analog; TSA; isostere; gpl20; HIV-1; T-helper;
KW tetanus; toxoid; B-T-epitope.

```

XX OS Clostridium tetani.  
XX PN WO9948925-A1.  
XX XX  
XX PD 30-SEP-1999.  
XX XX  
XX PF 23-MAR-1999; 99WO-US06325.  
XX PR 23-MAR-1998; 98US-0046373.  
XX PA (UYNE-) UNIV NEBRASKA.  
XX PI Paul S, Gololobov G, Smith L;  
XX DR WPI; 1999-591076/50.  
XX PT New covalently reactive antigen analogs used for treating e.g.  
XX PT autoimmune diseases, lymphoproliferative disorders, cancers, microbial  
XX PT infections, ischemic and reperfusion injury or septic shock -  
XX PS Disclosure; Page 86; 158pp; English.  
XX CC The patent discloses new covalently reactive antigen analogs (CRAA)  
XX CC of formula XI-Y-E-X2, in which XI and X2 represent peptide sequences  
XX CC of an epitope of a disease-associated protein, Y is a positively  
XX CC charged amino acid residue, preferably Lys or Arg, and E is an  
XX CC electrophilic reaction centre, preferably a phosphonate or boronate  
XX CC moiety. Depending on the identity of the epitope, the CRAA may be used  
XX CC to stimulate production of catalytic antibodies specific for  
XX CC predetermined antigens associated with particular medical disorders.  
XX CC They may also be used to permanently inactivate endogenously produced  
XX CC catalytic antibodies produced in certain autoimmune diseases as well as  
XX CC in certain lymphoproliferative disorders.  
XX CC Amongst the specifically exemplified CRAAs is one based on residues  
XX CC 421-436 of a B-cell epitope of gp120 (see AAY04046) which may be used  
XX CC to counter HIV-1 infections. When used as an immunogen, preferably this  
XX CC CRAA is conjugated at its N-terminal to a T-helper epitope from tetanus  
XX CC toxoid. The present sequence represents the T-helper epitope and  
XX CC corresponds to residues 830-844 of the toxoid.  
XX SQ Sequence 15 AA;  
Query Match 100.0%; Score 74; DB 20; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15  
DB 1 qyikanskfigitel 15  
RESULT 7  
AAW67578  
ID AAW67578 standard; peptide; 15 AA.  
XX AC  
XX AC AAW67578;  
XX DT 02-MAR-1999 (first entry)  
XX DE T-cell epitope peptide #4 for chimeric fimbrin/T-cell epitope peptide.  
XX KW Chimeric; non-typable Haemophilus influenzae; fimbrin; T-cell epitope;  
XX KW immunogenic composition; immune response.  
XX OS Synthetic.  
XX OS US5843464-A.  
XX PN  
XX PD 01-DEC-1998.  
XX PF 02-JUN-1995; 95US-0460502.

XX PR 02-JUN-1995; 95US-0460502.  
XX PA (OHIS ) UNIV OHIO STATE.  
XX PI Bakaletz LO, Kaumaya PTP;  
XX DR WPI; 1999-044514/04.  
XX XX Synthetic chimeric fimbrin peptide - useful for vaccination against  
XX PT non-typable Haemophilus influenzae  
XX PS Disclosure; Column 4; 16pp; English.  
XX CC The invention relates to the manufacture of a synthetic chimeric peptide  
XX CC comprising a non-typable Haemophilus influenzae fimbrin peptide fused via  
XX CC a linker peptide to a T-cell epitope peptide. The chimeric peptide is  
XX CC used in immunogenic compositions which induce an immune response against  
XX CC non-typable Haemophilus influenzae. This sequence represents an example  
XX CC of a T-cell epitope peptide used to generate the chimeric peptide.  
XX SQ Sequence 15 AA;  
Query Match 100.0%; Score 74; DB 20; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15  
DB 1 qyikanskfigitel 15  
RESULT 8  
AAW73220  
ID AAW73220 standard; Protein; 15 AA.  
XX AC  
XX AC AAW73220;  
XX DT 25-JAN-1999 (first entry)  
XX DE Tetanus toxoid epitope.  
XX KW Multispecific single chain antibody; antibody H22; tumour cell; therapy;  
XX KW antibody-dependent cellular cytotoxicity; ADCC; HER 2/neu; infection;  
XX KW epidermal growth factor receptor; breast cancer; ovarian cancer.  
XX OS Synthetic.  
XX OS US5837243-A.  
XX PD 17-NOV-1998.  
XX PF 07-JUN-1996; 96US-0661052.  
XX PR 07-JUN-1996; 96US-0661052.  
XX PR 07-JUN-1995; 95US-0484172.  
XX PA (MEDA-) MEDAREX INC.  
XX PI Deo YM, Goldstein J, Graziano R, Somasundaram C;  
XX DR WPI; 1999-023374/02.  
XX XX Specific killing of tumour cells - using a multi-specific molecule  
XX PT comprising an anti-Fc receptor antibody and a portion which binds to  
XX PT a target cell  
XX PS Example 7; Column 27; 57pp; English.  
XX CC This sequence represents a tetanus toxoid epitope and is recognised  
XX CC by the multispecific single chain antibody designated H22. The  
XX CC antibody can be used in the method of the invention for inducing



Query Match 100.0%; Score 74; DB 21; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15  
 | | | | | | | | | | | | | | |  
 Db 1 qyikanskfigitel 15

## RESULT 11

AA92625  
 ID AAY92625 standard; Protein; 15 AA.

XX AC AAY92625;  
 XX DT 10-AUG-2000 (first entry)  
 XX DE Foreign epitope P2.  
 XX KW Foreign epitope; P2; prostate specific membrane antigen; PSM; Her2;  
 KW Heregulin 2; Fibroblast growth factor 8b; FGF8b; vaccination;  
 KW cytotoxic T-lymphocyte immunity; self-protein; cancer; breast cancer;  
 KW prostate cancer; cell-associated peptide antigen.

XX OS Clostridium tetani.

XX PN WO200020027-A2.

XX PD 13-APR-2000.

XX PF 05-OCT-1999; 99WO-DK00525.

XX PR 05-OCT-1998; 98DK-0001261.

XX PR 20-OCT-1998; 98US-0105011.

XX PA (MEBI-) M & E BIOTECH AS.

XX PI Steinaa L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;  
 PI Gautam A, Birk P, Karlsson G;

XX DR WPI: 2000-349917/30.

XX DR N-PSDB; AAA09460.

XX PT Inducing immune responses to weakly immunogenic, tumor associated  
 PT peptide antigens for the treatment of breast and prostate cancer

XX PS Example 1; Page 213; 220pp; English.

XX CC The claims detail a method for inducing immune responses against weakly  
 CC immunogenic cell-associated peptide antigens (PA) such as those  
 CC associated with cancers (i.e. self-proteins), for example, human  
 CC prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or  
 CC fibroblast growth factor 8b (FGF8b). The method comprises effecting  
 CC simultaneous presentation by antigen producing cells (APCs) of the  
 CC animal's immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte)  
 CC group derived from the PA and/or at least 1 B-cell group derived from the  
 CC cell-associated PA; and (2) at least 1 first T helper cell group which is  
 CC foreign to the animal. Analogues of human PSM, human Her2 and  
 CC human/murine FGF8b comprising a substantial part of all known and  
 CC predicted CTL and B-cell epitopes of the respective PA and including at  
 CC least one foreign T helper epitope (e.g. P2 and/or P30) are also claimed.  
 CC The method is used to treat prostate, prostate/breast or breast cancer  
 CC when the PA is human PSM, FGF8b and Her2, respectively.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 21; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15  
 | | | | | | | | | | | | | | |

Db 1 qyikanskfigitel 15

## RESULT 12

AA984427  
 ID AAY84427 standard; Peptide; 15 AA.

XX AC AAY84427;

XX DT 25-JUL-2000 (first entry)

XX DE Amino acid sequence of the tetanus toxoid P2 epitope.

XX KW Osteoprotegerin ligand; OPG; osteoprotegerin; osteoclastogenesis;  
 KW tumour necrosis factor receptor; type II transmembrane protein;  
 KW osteoclast differentiation; CSF-1; osteoclast activator;  
 KW immune response; osteoporosis; bone resorption;  
 KW tetanus toxoid P2 epitope.

XX OS Clostridium tetani.

XX PN WO200015807-A1.

XX PD 23-MAR-2000.

XX PF 13-SEP-1999; 99WO-DK00481.

XX PR 15-SEP-1998; 98DK-0001164.

XX PR 02-OCT-1998; 98US-0102896.

XX PA (MEBI-) M & E BIOTECH AS.

XX PI Halkier T, Haaning J;

XX DR WPI: 2000-271444/23.

XX PT In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used  
 PT to treat, prevent and ameliorate osteoporosis -

XX PS Example; Page 106; 110pp; English.

XX CC The present sequence represents the tetanus toxoid P2 epitope. It is  
 CC used to create a fusion protein with murine osteoprotegerin ligand  
 CC (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis  
 CC factor receptor family, which blocks osteoclastogenesis in a dose  
 CC dependent manner. The OPGL protein is synthesised as a type II  
 CC transmembrane protein. The murine and human OPGL polypeptides are 87%  
 CC homologous. OPGL is a potent osteoclast differentiation factor when  
 CC combined with CSF-1. It is not capable of inducing osteoclast  
 CC differentiation in the absence of CSF-1. OPGL is also an activator of  
 CC mature osteoclasts. The specification describes a method for the in vivo  
 CC down-regulation of OPGL activity in an animal. The method comprises  
 CC using at least one OPGL polypeptide or subsequence, and/or at least one  
 CC OPGL analogue to induce an immune response in the animal. The method  
 CC and OPGL polypeptide are useful for treating, preventing and ameliorating  
 CC osteoporosis or other diseases or conditions characterised by excessive  
 CC bone resorption.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 21; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15  
 | | | | | | | | | | | | | | |

Db 1 qyikanskfigitel 15

## RESULT 13

AA970300  
 ID AAY70300 standard; peptide; 15 AA.



```

XX AC AAY70300;
XX
XX DT 06-JUN-2000 (first entry)
XX
XX DE Clostridium tetani tetanus toxoid T-cell epitope, P589.
XX
XX KW Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine;
XX T-cell epitope; tetanus toxoid; antigenic epitope; treatment;
XX KW circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2;
XX KW liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2;
XX KW apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175;
XX KW EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen;
XX KW Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.
XX
XX OS Clostridium tetani.
XX
XX PN WO20001179-A1.
XX
XX PD 02-MAR-2000.
XX
XX PF 19-AUG-1999; 99WO-US18869.
XX
XX PR 21-AUG-1998; 98US-0097703.
XX
XX PA (NAIM-) NAT INST IMMUNOLOGY.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Lal AA, Shi YP, Hasnain SE;
XX
XX DR WPI; 2000-237654/20.
XX
XX PT Novel recombinant protein as vaccine for treating malarial infection
XX PT comprises antigenic peptides obtained from different stages of
XX PT plasmodium falciparum life cycle -
XX
XX PS Claim 2; Page 17; 52pp; English.
XX
XX CC The present sequence is the tetanus toxoid T-cell epitope P589, derived
XX CC from Clostridium tetani. It is used in the construction of recombinant
XX CC protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial
XX CC vaccine. The recombinant protein comprises, melittin signal peptide,
XX CC (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes
XX CC from circumsporozoite protein (CSP), sporozoite surface protein-2
XX CC (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1
XX CC (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding
XX CC antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete
XX CC specific antigen, Pfg27. These epitopes were obtained at different stages
XX CC of the life cycle of P. falciparum. CDC/NIIMALVAC-1 vaccine has
XX CC antiparasitic activity and can used for treatment and prevention of
XX CC malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for
XX CC detecting P. falciparum in biological samples.
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 100.0%; Score 74; DB 21; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-07;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 QYIKANSKFIGITEL 15
XX | | | | | | | | | |
XX Db 1 qvikanskfigitel 15
XX
XX RESULT 14
XX AAY44763
XX ID AAY44763 standard; peptide; 15 AA.
XX
XX AC AAY44763;
XX
XX DT 04-MAY-2000 (first entry)
XX
XX KW HER 2/neu; epidermal growth factor receptor; EGFR; multispecific protein;

```

```

DE XX Tetanus toxoid protein derived T-cell activating epitope P2.
KW XX Surface layer protein; S-layer secretion signal; antibiotic; vaccine;
KW KW recombinant fusion protein cleavage; enzyme; protein polymer; foodstuff;
KW KW antibacterial enzyme; surface glycoprotein; T-cell activating epitope;
KW KW P2; tetanus toxoid; IPNV; Infectious pancreatic necrosis virus.
XX
XX OS Clostridium tetani.
XX
XX PN WO200004170-A1.
XX
XX PD 27-JAN-2000.
XX
XX PF 14-JUL-1999; 99WO-CA000637.
XX
XX PR 14-JUL-1998; 98CA-2237704.
XX
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX PI Smit J;
XX
XX DR WPI; 2000-182434/16.
XX
XX PT Cleavage of Caulobacter produced recombinant fusion proteins useful for
XX PT producing vaccine peptides -
XX
XX PS Example 2; Page 16; 33pp; English.
XX
XX CC The patent discloses a method for cleaving a recombinant fusion protein
XX CC which is produced by Caulobacter and consists of Caulobacter surface
XX CC layer (S-layer) protein (containing the C-terminal secretion signal) and
XX CC a target protein heterologous to Caulobacter. The cleavage of target
XX CC protein from the S-layer protein is carried out under mild acid
XX CC conditions so that cleavage occurs at aspartate-proline dipeptide site
XX CC without solubilising the protein. The cleavage is accomplished while the
XX CC fusion protein is in an insoluble aggregate form which facilitates
XX CC purification of the protein. The method is useful for producing pure
XX CC proteins including recombinant human and animal therapeutic antibiotic
XX CC and vaccine peptides, enzymes, protein polymers, and antibacterial
XX CC enzymes for foodstuffs.
XX CC The present sequence is a T-cell activating epitope P2 derived
XX CC from tetanus toxoid protein. This sequence was fused to a DNA encoding
XX CC a fragment of Infectious pancreatic necrosis virus surface glycoprotein
XX CC which is a vaccine candidate. This chimeric protein was in turn fused to
XX CC DNA encoding C. crescentus S-layer secretion signal (corresponds to the
XX CC C-terminal portion of the S-layer protein from amino acid 690 onwards and
XX CC contains native Asp-Pro site) for construction of a recombinant
XX CC fusion construct which is expressed in Caulobacter and then cleaved
XX CC to recover the vaccine candidate protein.
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 100.0%; Score 74; DB 21; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-07;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 QYIKANSKFIGITEL 15
XX | | | | | | | | | |
XX Db 1 qvikanskfigitel 15
XX
XX RESULT 15
XX AAB85451
XX ID AAB85451 standard; peptide; 15 AA.
XX
XX AC AAB85451;
XX
XX DT 25-SEP-2001 (first entry)
XX
XX DE Wild-type TT830 (tetanus toxin) epitope.
XX
XX KW HER 2/neu; epidermal growth factor receptor; EGFR; multispecific protein;

```

KW Fc receptor; FcR; tumor cell; breast; cancer; sarcoma; carcinoma; HIV;  
KW pathogenic; Toxoplasma gondii; candidiasis; systemic lupus; cytostatic;  
KW immune thrombocytopenia purpura; immunosuppressive; antiviral;  
XX antifungal; antiprotozoal; TT830; tetanus toxin.

OS Clostridium tetani.

XX US6270765-B1.

XX 07-AUG-2001.

XX 06-NOV-1998; 98US-0188082.

XX 07-JUN-1996; 96US-0661052.

PR 07-JUN-1995; 95US-0484172.

XX (MEDA-) MEDAREX INC.

XX Deco YM, Goldstein J, Graziano R, Somasundaram C;

XX WPI; 2001-475189/51.

DR N-PSDB; AAH23378.

XX Inducing killing of tumor cells which expresses HER 2/neu or epidermal  
PT growth factor receptor (EGFR) by contacting the cell with multispecific  
PT proteins comprising an anti-Fc receptor, -Her 2/neu or -EGFR antibody,  
PT useful for treating cancer -

XX Example 7; Fig 24; 57pp; English.

XX The invention relates to a new method for inducing killing of a tumor  
CC cell which expresses HER 2/neu or epidermal growth factor receptor  
CC (EGFR). The method comprises contacting the tumor cell with a  
CC multispecific protein comprising a component, preferably an antibody,  
CC which binds to an Fc receptor (FcR), Her 2/neu or EGFR. The method is  
CC useful for inducing killing of a tumor cell from breast cancer, sarcoma,  
CC carcinoma, or ovarian cancer. Specific multispecific proteins can also be  
CC administered to a subject to treat or prevent other diseases or  
CC conditions, including pathogenic infections (e.g., viral (such as HIV)),  
CC protozoan infections (such as Toxoplasma gondii), fungal infections  
CC (such as candidiasis), and an autoimmunity (e.g. immune thrombocytopenia  
CC purpura and systemic lupus). The present sequence represents a wild-type  
CC tetanus toxin TT830 epitope.

XX Sequence 15 AA;

Query Match 100.0%; Score 74; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIRANSKFIGITEL 15  
| | | | | | | | | | | | | | |  
Db 1 qyikanskfigitel 15

Search completed: January 29, 2002, 10:59:20  
Job time: 2244 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 29, 2002, 10:59:58 ; Search time 32.24 Seconds  
(without alignments)  
10.470 Million cell updates/sec

Title: us-09-763-397A-24

Perfect score: 74

Sequence: 1 QYIKANSKFIGITEL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued\_Patents\_AA.\*  
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2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	15	2	US-08-319-704-10
2	74	100.0	15	2	US-08-661-052-6
3	74	100.0	15	2	US-08-460-502-7
4	74	100.0	15	4	US-09-046-373-2
5	74	100.0	15	4	US-09-188-082-6
6	74	100.0	15	5	PCT-US93-11703-69
7	74	100.0	16	4	US-09-248-588-55
8	74	100.0	17	1	US-08-446-692-4
9	74	100.0	17	2	US-08-488-351A-4
10	74	100.0	17	3	US-09-100-409A-40
11	74	100.0	17	5	PCT-US95-08596-23
12	74	100.0	17	5	PCT-US95-13841-7
13	74	100.0	27	1	US-08-446-692-13
14	74	100.0	27	2	US-08-488-351A-13
15	74	100.0	31	5	PCT-US93-11703-63
16	74	100.0	37	1	US-08-446-692-57
17	74	100.0	37	1	US-08-446-692-63
18	74	100.0	37	2	US-08-488-351A-57
19	74	100.0	37	2	US-08-488-351A-63
20	74	100.0	47	1	US-08-446-692-35
21	74	100.0	47	2	US-08-488-351A-35
22	70	94.6	14	1	US-08-186-266-5
23	70	94.6	14	1	US-08-305-871A-5
24	70	94.6	14	1	US-08-465-167A-18
25	70	94.6	14	2	US-08-817-933A-9
26	70	94.6	14	5	PCT-US92-07218-15
27	70	94.6	14	5	PCT-US92-07218-30

28	70	94.6	14	5	PCT-US95-02121-95	Sequence 95, Appl
29	70	94.6	24	5	PCT-US92-07218-25	Sequence 25, Appl
30	70	94.6	24	5	PCT-US92-07218-31	Sequence 31, Appl
31	70	94.6	27	5	PCT-US95-02121-110	Sequence 110, App
32	70	94.6	27	5	PCT-US92-07218-26	Sequence 26, Appl
33	70	94.6	27	5	PCT-US92-07218-27	Sequence 27, Appl
34	70	94.6	27	5	PCT-US92-07218-28	Sequence 28, Appl
35	70	94.6	27	5	PCT-US92-07218-32	Sequence 32, Appl
36	70	94.6	27	5	PCT-US95-02121-111	Sequence 111, App
37	70	94.6	27	5	PCT-US95-02121-112	Sequence 112, App
38	70	94.6	29	3	US-09-075-257A-13	Sequence 13, Appl
39	70	94.6	29	3	US-09-075-257A-14	Sequence 14, Appl
40	70	94.6	29	4	US-09-534-639-13	Sequence 13, Appl
41	70	94.6	29	4	US-09-534-639-14	Sequence 14, Appl
42	70	94.6	30	5	PCT-US92-07218-29	Sequence 29, Appl
43	70	94.6	32	1	US-08-186-266-9	Sequence 9, Appl
44	70	94.6	50	4	US-09-171-969-7	Sequence 7, Appl
45	69	93.2	15	2	US-08-661-052-9	Sequence 9, Appl

#### ALIGNMENTS

RESULT 1  
US-08-319-704-10  
; Sequence 10, Application US/08319704  
; Patent No. 5814617  
; GENERAL INFORMATION:  
; APPLICANT: Hoffman, Stephen L.  
; APPLICANT: Charoenvit, Yupin  
; APPLICANT: Hedstrom, Richard C.  
; APPLICANT: Doolan, Denise L.  
; TITLE OF INVENTION: Protective 17 kDa Malaria Hepatic and  
; TITLE OF INVENTION: Erythrocytic Stage Immunogen and Gene  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Naval Medical R & D Command  
; STREET: Bldg 1, T-12, 8901 Wisconsin Avenue  
; CITY: Bethesda  
; STATE: Maryland  
; COUNTRY: U.S.A.  
; ZIP: 20889-5606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/319,704  
; FILING DATE: 07-OCT-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: A. David Spevack  
; REGISTRATION NUMBER: 24,743  
; REFERENCE/DOCKET NUMBER: 75,206  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 295-6759  
; TELEFAX: (301) 295-1022  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-319-704-10

Query Match 100.0%; Score 74; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15  
|||||

Db 1 QYIKANSKFIGITEL 15

RESULT 2

US-08-661-052-6

Sequence 6, Application US/08661052

Patent No. 5837243

GENERAL INFORMATION:

APPLICANT: Yashwant M. Deo

APPLICANT: Joel Goldstein

APPLICANT: Robert Graziano

APPLICANT: Chезian Somasundaram

TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED

TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/661,052

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/484,172

FILING DATE: 07-JUNE-1995

ATTORNEY/AGENT INFORMATION:

NAME: Arnold, Beth E.

REGISTRATION NUMBER: 35,430

REFERENCE/DOCKET NUMBER: MXI-043CP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

US-08-661-052-6

Query Match 100.0%; Score 74; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15

Db 1 QYIKANSKFIGITEL 15

RESULT 3

US-08-460-502-7

Sequence 7, Application US/08460502

Patent No. 5843464

GENERAL INFORMATION:

APPLICANT: Bakaletz, Lauren O.

APPLICANT: Kaumaya, Parvin T.

TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Calfee, Halter and Griswold

STREET: 800 Superior Avenue

CITY: Cleveland

STATE: Ohio

US-08-460-502-7

Query Match 100.0%; Score 74; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15

Db 1 QYIKANSKFIGITEL 15

RESULT 4

US-09-046-373-2

Sequence 2, Application US/09046373

Patent No. 6235714

GENERAL INFORMATION:

APPLICANT: Sudhir Paul

APPLICANT: Larry J. Smith

APPLICANT: Gennady Gololobov

TITLE OF INVENTION: Methods for Identifying Inducers and

TITLE OF INVENTION: Inhibitors of Catalytic Antibodies, Compositions and Their

TITLE OF INVENTION: Use

FILE REFERENCE: UNMC 63123

CURRENT APPLICATION NUMBER: US/09/046,373

CURRENT FILING DATE: 1998-03-23

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 15

TYPE: PRT

ORGANISM: Clostridium tetani

US-09-046-373-2

Query Match 100.0%; Score 74; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15

Db 1 QYIKANSKFIGITEL 15

RESULT 5

US-09-188-082-6

Sequence 6, Application US/09188082

Patent No. 6270765

US-09-188-082-6

Query Match 100.0%; Score 74; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15

Db 1 QYIKANSKFIGITEL 15

RESULT 5

US-09-188-082-6

Sequence 6, Application US/09188082

Patent No. 6270765

GENERAL INFORMATION:  
APPLICANT: Yashwant M. Deo  
APPLICANT: Joel Goldstein  
APPLICANT: Robert Graziano  
APPLICANT: Chezian Somsundaram  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
OF ANTI-FC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/188,082  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/661,052  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-09-188-082-6

Query Match 100.0%; Score 74; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OYIKANSKFIGITEL 15  
Db 1 OYIKANSKFIGITEL 15

RESULT 6  
PCT-US93-11703-69  
GENERAL INFORMATION:  
APPLICANT: Chiron Mimotopes Pty. Ltd.  
TITLE OF INVENTION: T-Cell Epitopes  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Grant D. Green  
STREET: 4560 Horton St.  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/11703

FILING DATE: 28-DEC-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/984,852  
FILING DATE: 02-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Green, Grant D.  
REGISTRATION NUMBER: 31,259  
REFERENCE/DOCKET NUMBER: 0222.101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-601-2706  
TELEFAX: 510-655-3542  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-11703-69

Query Match 100.0%; Score 74; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OYIKANSKFIGITEL 15  
Db 1 OYIKANSKFIGITEL 15

RESULT 7  
US-09-248-588-55  
Sequence 55, Application US/09248588  
Patent No. 6231864  
GENERAL INFORMATION:  
APPLICANT: Birkett, Ashley J.  
TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and  
their Derivatives  
FILE REFERENCE: SYN-101 4564/69529  
CURRENT APPLICATION NUMBER: US/09/248,588  
CURRENT FILING DATE: 1999-02-11  
EARLIER APPLICATION NUMBER: 60/074537  
EARLIER FILING DATE: 1998-02-12  
NUMBER OF SEQ ID NOS: 113  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 55  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Clostridium tetani  
PUBLICATION INFORMATION:  
JOURNAL: Vaccine  
VOLUME: 15  
ISSUE: 4  
PAGES: 377-  
DATE: 1997  
US-09-248-588-55

Query Match 100.0%; Score 74; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OYIKANSKFIGITEL 15  
Db 1 OYIKANSKFIGITEL 15

RESULT 8  
US-08-446-692-4  
Sequence 4, Application US/08446692  
Patent No. 5759551  
GENERAL INFORMATION:

APPLICANT: Ladd, Anna  
APPLICANT: Wang, Chang Yi  
APPLICANT: Zamb, Timothy  
TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Maria C.H. Lin  
STREET: 345 Park Avenue  
CITY: New York  
STATE: NY  
COUNTRY: US  
ZIP: 10154-0053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,692  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maria C.H. Lin  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 1151-4146 US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)415-8745  
TELEFAX: (516)751-6849  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-446-692-4

Query Match 100.0%; Score 74; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15  
Db 3 QYIKANSKFIGITEL 17  
RESULT 9  
US-08-488-351A-4  
Sequence 4, Application US/08488351A  
Patent No. 5843446  
GENERAL INFORMATION:  
APPLICANT: Ladd, Anna  
APPLICANT: Wang, Chang Yi  
APPLICANT: Zamb, Timothy  
TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Maria C.H. Lin  
STREET: 345 Park Avenue  
CITY: New York  
STATE: NY  
COUNTRY: US  
ZIP: 10154-0053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,351A  
FILING DATE: 7-JUN-1995

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/446,692  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/229,275  
FILING DATE: 14-APR-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,166  
FILING DATE: 27-APR-1992  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maria C.H. Lin  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 1151-4146 US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)415-8745  
TELEFAX: (516)751-6849  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-488-351A-4

Query Match 100.0%; Score 74; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15  
Db 3 QYIKANSKFIGITEL 17

RESULT 10  
US-09-100-409A-40  
Sequence 40, Application US/09100409A  
Patent No. 6090388  
GENERAL INFORMATION:  
APPLICANT: Wang, Chang Yi  
TITLE OF INVENTION: PEPTIDE COMPOSITION FOR  
PREVENTION AND TREATMENT OF HIV INFECTION AND  
IMMUNE DISORDERS  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 Park Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10154-0054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version  
#1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/100,409A  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME:  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 1151-4154  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
INFORMATION FOR SEQ ID NO: 40:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-100-409A-40

Query Match 100.0%; Score 74; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15  
| | | | | | | | | | | | | | | | |  
Db 3 QYIKANSKFIGITEL 17

RESULT 11  
PCT-US95-08596-23  
; Sequence 23, Application PC/TUS9508596  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Proinsulin Peptide Compounds for Detecting  
; and treating Type I Diabetes  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/08596  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/272,220  
; FILING DATE: 08-JULY-1994  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A., Jr.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: DCI-092PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
PCT-US95-08596-23

Query Match 100.0%; Score 74; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15  
| | | | | | | | | | | | | | | | |  
Db 3 QYIKANSKFIGITEL 17

RESULT 12  
PCT-US95-13841-7

; Sequence 7, Application PC/TUS9513841  
; GENERAL INFORMATION:  
; APPLICANT: United Biomedical Inc; Walfield, Alan M.;  
; APPLICANT: Wang, Chang Yi  
; TITLE OF INVENTION: Synthetic IgE Membrane Anchor  
; TITLE OF INVENTION: Peptide Immunogens for the Treatment of Allergy  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Maria C.H. Lin  
; STREET: 345 Park Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/13841  
; FILING DATE: 25-OCT-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/328,519  
; FILING DATE: 25-OCT-1994  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lin, Maria C.H.  
; REGISTRATION NUMBER: 29,323  
; REFERENCE/DOCKET NUMBER: 1151-4117  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-758-4800  
; TELEFAX: 212-751-6849  
; TELEX: 421792  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
PCT-US95-13841-7

Query Match 100.0%; Score 74; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15  
| | | | | | | | | | | | | | | | |  
Db 3 QYIKANSKFIGITEL 17

RESULT 13  
US-08-446-692-13  
; Sequence 13, Application US/08446692  
; Patent No. 5759551  
; GENERAL INFORMATION:  
; APPLICANT: Ladd, Anna  
; APPLICANT: Wang, Chang Yi  
; APPLICANT: Zamb, Timothy  
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Maria C.H. Lin  
; STREET: 345 Park Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: US  
; ZIP: 10154-0053  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

Db 10 QYIKANSKFIGITEL 24



Search completed: January 29, 2002, 10:59:58  
Job time: 2144 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 11:00:40 ; Search time 34.94 Seconds  
(without alignments)  
32.702 Million cell updates/sec

Title: US-09-763-397A-24

Perfect score: 74

Sequence: 1 QYIKANSKFIGITEL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68:\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	1315	1 BRLTN	tentoxylisin (EC 3
2	44.5	60.1	244	2 S29982	class II histocomp
3	44	59.5	66	2 S31029	gene 84 protein -
4	43	58.1	180	2 G68826	diamine N-acetyltr
5	43	58.1	899	2 T42976	hypothetical prote
6	42.5	57.4	1060	2 S06286	major merizoite su
7	42.5	57.4	1086	2 S16752	major merizoite su
8	42.5	57.4	1701	2 A54498	major merizoite su
9	42.5	57.4	1701	2 A26868	major merizoite su
10	42.5	57.4	1726	1 SAZQGM	major merizoite su
11	42.5	57.4	1726	2 A45948	major merizoite su
12	42	56.8	1333	2 S38635	blastopia polyprot
13	41	55.4	123	2 G48677	Ig heavy chain v-D
14	41	55.4	899	2 G36812	hypothetical prote
15	40.5	54.7	245	2 S29980	class II histocomp
16	40	54.1	79	2 D85794	hypothetical prote
17	40	54.1	194	2 G64026	lacyl-carrier-prot
18	40	54.1	601	1 A55485	oligopeptidase (EC
19	40	54.1	601	2 G86840	oligoendopeptidase
20	40	54.1	644	2 S46746	hypothetical prote
21	39	52.7	102	2 PH1491	Ig heavy chain v r
22	39	52.7	119	2 PH1516	Ig heavy chain v r
23	39	52.7	119	2 PH1518	Ig heavy chain v r
24	39	52.7	119	2 PH1519	Ig heavy chain v r
25	39	52.7	123	2 F48677	Ig heavy chain v-D
26	39	52.7	135	2 PH1494	Ig heavy chain v r
27	39	52.7	140	2 PH1488	Ig heavy chain v r
28	39	52.7	213	1 K1YMC	adenylate kinase (
29	39	52.7	326	2 B71808	type II restrictio

#### RESULT 1

BRLTN

tentoxylisin (EC 3.4.24.68) precursor - Clostridium tetani

N:Alternate names: tetanus neurotoxin

C:Species: Clostridium tetani

C:Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text change 18-Jun-1999

C:Accession: A25689; A25757; A25194; B25194; A60759; S69348; S09364

R:Eisel, U.; Jarausch, W.; Goretzki, K.; Henschen, A.; Engels, J.; Weller, U.; Hudel, EMBO J. 5, 2495-2502, 1986

A:Title: Tetanus toxin: primary structure, expression in E. coli, and homology with b

A:Reference number: A25689; MUID:87053814

A:Accession: A25689

A:Molecule type: DNA

A:Residues: 1-1315 <EIS>

A:Cross-references: GB:X04436; NID:g40769; PIDN:CAA28033.1; PID:g40770

R:Fairweather, N.F.; Lyness, V.A.

Nucleic Acids Res. 14, 7809-7812, 1986

A:Title: The complete nucleotide sequence of tetanus toxin.

A:Reference number: A25757; MUID:87040747

A:Accession: A25757

A:Molecule type: DNA

A:Residues: 1-1315 <FAI>

A:Cross-references: GB:X06214; NID:g40773; PIDN:CAA29564.1; PID:g40774

A:Experimental source: strain CN3911

R:Fairweather, N.F.; Lyness, V.A.; Pickard, D.J.; Allen, G.; Thomson, R.O.

J. Bacteriol. 165, 21-27, 1986

A:Title: Cloning, nucleotide sequencing, and expression of tetanus toxin fragment C 1

A:Reference number: A25194; MUID:86085672

A:Accession: A25194

A:Molecule type: DNA

A:Residues: 743-1315 <FA2>

A:Cross-references: GB:M12739; NID:gl44920; PIDN:AAA23282.1; PID:gl44921

A:Accession: B25194

A:Molecule type: protein

R:Matsuda, M.; Iel, D.I.; Sugimoto, N.; Ozutsumi, K.; Okabe, T.

Infect. Immun. 57, 3588-3593, 1989

A:Title: Isolation, purification, and characterization of fragment B, the NH-2-termin

A:Reference number: A60759; MUID:90035436

A:Accession: A60759

A:Molecule type: protein

A:Residues: 461-475 <WAT>

R:Demotz, G.; Lanzavecchia, L.; Eisel, U.; Niemann, H.; Widmann, C.; Corradin, G.

J. Immunol. 142, 394-402, 1989

A:Title: Delineation of several DR-restricted tetanus toxin T cell epitopes.

A:Reference number: JS0098; MUID:89093918

A:Contents: annotation; epitope region

R:Schlavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta,

Nature 359, 832-835, 1992

A:Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteo

A:Reference number: S27125; MUID:93063293

A:Contents: annotation

R:de Filippis, V.; Vangelista, L.; Schiavo, G.; Tonello, F.; Montecucco, C.  
Eur. J. Biochem. 229, 61-69, 1995  
A:Title: Structural studies on the zinc-endopeptidase light chain of tetanus neurotoxin.  
A:Reference number: S69348; MUID:95262688  
A:Accession: S69348  
A:Molecule type: protein  
A:Residues: 2-31 <DEF>  
C:Comment: The source of this protein was an extrachromosomal plasmid.  
C:Comment: The precursor is cleaved by endogenous proteinase activity to form light (fra  
dual chains are not toxic when separated). The amino end of the heavy chain (fragment B)  
C:Comment: Fragment B forms ion channels in a lipid bilayer. Fragment C binds to ganglio  
C:Comment: This potent neurotoxin binds to peripheral neuronal synapses, is internalized  
presynaptic neurons. It inhibits neurotransmitter release by proteolytic cleavage of sy  
C:Function:  
A:Description: blocks neuroexocytosis via hydrolysis of a Gln-Phe peptide bond in synapt  
C:Superfamily: tetanus toxin  
C:Keywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc  
F:2-457/Product: tetroxylisin light chain (fragment A) #status predicted <TTL>  
F:461-1315/Product: tetroxylisin heavy chain (fragment B.C) #status experimental <TTH>  
F:461-864/Domain: channel forming (fragment B) #status predicted <TXB>  
F:865-1315/Domain: ganglioside binding (fragment C) #status predicted <TXC>  
F:233,237/Binding site: zinc (His) #status predicted  
F:234/Active site: Glu #status predicted

Query Match 100.0%; Score 74; DB 1; Length 1315;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15  
|||||  
Db 830 QYIKANSKFIGITEL 844

RESULT 2  
S29982  
class II histocompatibility antigen - Atlantic salmon  
C:Species: Salmo salar (Atlantic salmon)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Sep-1999  
C:Accession: S29982  
R:Hardvik, I.  
submitted to the EMBL Data Library, October 1992  
A:Reference number: S29980  
A:Accession: S29982  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-244 <HOR>  
A:Cross-references: EMBL:X70166; NID:g64369; PID:g64370  
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 60.1%; Score 44.5; DB 2; Length 244;  
Best Local Similarity 55.6%; Pred. No. 1.4;  
Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 1 QYIKANS---KFIGITEL 15  
:||: || ||: |||  
Db 51 EYIRFNSTVGKFGVGYTEL 68

RESULT 3  
S31029  
gene 84 protein - Mycobacterium phage L5  
C:Species: Mycobacterium phage L5  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 08-Oct-1999  
C:Accession: S31029  
R:Donnelly-Wu, M.K.; Jacobs Jr., W.R.; Hatfull, G.F.  
Mol. Microbiol. 7, 407-417, 1993  
A:Title: Superinfection immunity of mycobacteriophage L5: applications for genetic trans  
A:Reference number: S30949; MUID:93211283  
A:Accession: S31029  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA

A:Residues: 1-66 <DON>  
A:Cross-references: EMBL:Z18946; NID:g15859; PIDN:CAA79460.1; PID:e59702; PID:g579152  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992  
C:Genetics: 84  
A:Gene: 84  
A:Start codon: GTG

Query Match 59.5%; Score 44; DB 2; Length 66;  
Best Local Similarity 57.1%; Pred. No. 0.45;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 YIKANSKFIGITEL 15  
||| ||: ||: ||:  
Db 50 YIKRNGKFGVTWEV 63

RESULT 4  
G86826  
diamine N-acetyltransferase (EC 2.3.1.57) [imported] - Lactococcus lactis subsp. lact  
N:Alternate names: spermidine acetyltransferase  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 04-Apr-2001  
C:Accession: G86826  
R:Botolin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh  
Genome Res. in press, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium.  
A:Reference number: A86625  
A:Accession: G86826  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-180 <STO>  
A:Cross-references: GB:AE005176; NID:gl2724622; PIDN:AAK05713.1; GSPDB:GN00146  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: YGFF  
C:Keywords: acyltransferase; coenzyme A

Query Match 58.1%; Score 43; DB 2; Length 180;  
Best Local Similarity 69.2%; Pred. No. 1.9;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 IKANSKFIGITEL 15  
|-|| |||| ||  
Db 65 IEANDFIGIVEL 77

RESULT 5  
T42976  
hypothetical protein 63 - ateline herpesvirus 3 (strain 73)  
C:Species: ateline herpesvirus 3  
A:Variety: Strain 73  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jan-2000  
C:Accession: T42976  
R:Albrecht, J.C.; Fleckenstein, B.  
submitted to the EMBL Data Library, August 1998  
A:Description: Primary structure of the herpesvirus ateles genome.  
A:Reference number: Z22274  
A:Accession: T42976  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-899 <ALB>  
A:Cross-references: EMBL:AF083424; PIDN:AAC95587.1  
A:Experimental source: strain 73

Query Match 58.1%; Score 43; DB 2; Length 899;  
Best Local Similarity 64.3%; Pred. No. 9.9;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITE 14  
||| :|| || |||



Query Match	56.8%	Score 42;	DB 2;	Length 1333;
Best Local Similarity	53.3%;	Pred. No. 23;		
Matches	8; Conservative	3; Mismatches	4; Indels	0; Gaps 0;
QY	1 QYIKANSKFIGITEL	15		
	: ::			
Dd	127 KYVQARSKMIGSAEL	141		

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-245 <HOR>  
A:Cross-references: EMBL:X70167; NID:g64371; PID:g64372  
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 54.7%; Score 40.5; DB 2; Length 245;  
Best Local Similarity 44.4%; Pred. No. 7.6;  
Matches 8; Conservative 5; Mismatches 2; Indels 3; Gaps 1;

Qy 1 QYIKANS---KFIGITEL 15  
:|::||| |::|  
Db 53 EYVRFNSTVGKXVGYTEL 70

Search completed: January 29, 2002, 11:00:40  
Job time: 2030 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 29, 2002, 11:16:19 ; Search time 20.36 Seconds  
(without alignments)  
27.012 Million cell updates/sec

Title: US-09-763-397A-24

Perfect score: 74

Sequence: 1 QYIKANSKFIGITEL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	74	100.0	1314	1	TETX_CLOTE
2	44	59.5	66	1	VG84_BPM15
3	42.5	57.4	1682	1	MSP1_PLAF3
4	42.5	57.4	1701	1	MSP1_PLAFM
5	42.5	57.4	1701	1	MSP1_PLAFM
6	42.5	57.4	1726	1	MSP1_PLAF3
7	42.5	57.4	1726	1	MSP1_PLAFM
8	41	55.4	204	1	PYRC_SERMA
9	41	55.4	899	1	V120_HSVSA
10	40	54.1	194	1	ACPD_HAEIN
11	40	54.1	601	1	PEF1_LACLC
12	40	54.1	644	1	YHJ9_YEAST
13	39	52.7	213	1	KAD_MYCCA
14	38	51.4	256	1	YD83_METJA
15	38	51.4	287	1	TRUB_AQUAE
16	38	51.4	572	1	HEMA_P13HT
17	37	50.0	191	1	Y096_HAEIN
18	37	50.0	445	1	GNT1_HUMAN
19	37	50.0	447	1	GNT1_MOUSE
20	37	50.0	447	1	GNT1_RABIT
21	37	50.0	447	1	GNT1_RAT
22	37	50.0	490	1	Y032_BORBU
23	37	50.0	510	1	G6PD_ASPNG
24	37	50.0	511	1	G6PD_EMENI
25	37	50.0	548	1	YDD2_SCHPO
26	36	48.6	169	1	Y358_BUCAI
27	36	48.6	258	1	MIP_CHLPN
28	36	48.6	296	1	YD01_CLOBAB
29	36	48.6	333	1	DP08_XENLA
30	36	48.6	451	1	MURD_BACSU
31	36	48.6	461	1	NIFN_RHOCA
32	36	48.6	495	1	G6PD_PICJA
33	36	48.6	630	1	YND1_YEAST

## RESULT 1

ID	TETX_CLOTE	STANDARD;	PRT;	1314 AA.
AC	P04958;			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	TETANUS TOXIN PRECURSOR (EC 3.4.24.68) (TENTOXLYSIN).			
OS	Clostridium tetani.			
OG	Plasmid.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;			
OC	Clostridium.			
OX	NCBI_Taxid=1513;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87053814; PubMed=3536478;			
RA	Eisel U., Jarausch W., Goretzki K., Henschen A., Engels J.,			
RA	Weller U., Hudel M., Habermann E., Niemann H.;			
RT	"Tetanus toxin: primary structure, expression in E. coli, and			
RT	homology with botulinum toxins.";			
RL	EMBO J. 5:2495-2502(1986).			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CN3911;			
RX	MEDLINE=87040747; PubMed=3774547;			
RA	Fairweather N.F., Lyness V.A.;			
RT	"The complete nucleotide sequence of tetanus toxin.";			
RL	Nucleic Acids Res. 14:7809-7812(1986).			
RN	[3]			
RP	SEQUENCE OF 742-1314 FROM N.A.			
RX	MEDLINE=86085672; PubMed=3510187;			
RA	Fairweather N.F., Lyness V.A., Pickard D.J., Allen G., Thomson R.O.;			
RT	"Cloning, nucleotide sequencing, and expression of tetanus toxin			
RT	fragment C in Escherichia coli.";			
RL	J. Bacteriol. 165:21-27(1986).			
RN	[4]			
RP	PARTIAL SEQUENCE, AND DISULFIDE BONDS.			
RX	MEDLINE=90201034; PubMed=2108021;			
RA	Kriegstein K., Henschen A., Weller U., Habermann E.;			
RT	"Arrangement of disulfide bridges and positions of sulphhydryl groups			
RT	in tetanus toxin.";			
RL	Eur. J. Biochem. 188:39-45(1990).			
RN	[5]			
RP	PARTIAL SEQUENCE.			
RX	MEDLINE=92037649; PubMed=1935979;			
RA	Kriegstein K.G., Henschen A.H., Weller U., Habermann E.;			
RT	"Limited proteolysis of tetanus toxin. Relation to activity and			
RT	identification of cleavage sites.";			
RL	Eur. J. Biochem. 202:41-51(1991).			
RN	[6]			
RP	IDENTIFICATION AS ZINC-PROTEASE.			
RX	MEDLINE=93010948; PubMed=1396558;			
RA	Schiavo G., Poulain B., Rossetto O., Benfenati F., Tauc L.,			
RA	Montecucco C.;			
RT	"Tetanus toxin is a zinc protein and its inhibition of			
RT	neurotransmitter release and protease activity depend on zinc.";			

## ALIGNMENTS

34	36	48.6	774	1	RRP3_INCBE
35	36	48.6	774	1	RRP3_INCBJ
36	36	48.6	1630	1	MSP1_PLAFK
37	36	48.6	1639	1	MSP1_PLAFW
38	35	47.3	176	1	NUSC_SPIOL
39	35	47.3	261	1	CABV_CHICK
40	35	47.3	294	1	CDD_ECOLI
41	35	47.3	321	1	YDG7_SCHPO
42	35	47.3	329	1	DHOA_EMENI
43	35	47.3	353	1	41KD_LACHE
44	35	47.3	402	1	VGLD_HSVEA
45	35	47.3	431	1	Y4OP_RHISN

P21770	Influenza c
P13877	Influenza c
P04932	plasmodium
Q9m318	plasmodium
Q9m318	spinacia ol
P04354	gallus gall
P13652	escherichia
Q10494	schizosacch.
P25415	emericella
P17212	lactobacilli
P24872	equine herp
P55601	rhizobium s

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFITEL 15  
| | | | | | | | | |  
Db 829 QYIKANSKFITEL 843

RESULT 2  
VG84\_BPML5 VG84\_BPML5 STANDARD; PRT; 66 AA.  
AC Q05301;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last annotation update)  
DE GENE 84 PROTEIN (GP84).  
GN 84.

OS Mycobacteriophage L5.  
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.  
OX NCBI\_TaxID=31757;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93211282; PubMed=8459766;  
RA Hatfull G.F., Sarkis G.J.;  
RT "DNA sequence, structure and gene expression of mycobacteriophage L5:  
Rt a phage system for mycobacterial genetics."; Mol. Microbiol. 7:395-405(1993).

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CC -----  
DR EMBL; Z18946; CAA79460.1; - .  
DR PIR; S31029; S31029.  
SQ SEQUENCE 66 AA; 7424 MW; 9C7104C7A4FA74A5 CRC64;

Query Match 59.5%; Score 44; DB 1; Length 66;  
Best Local Similarity 57.1%; Pred. No. 0.2;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 YIKANSKFITEL 15  
| | | | | :  
Db 50 YIKRNGKFGVTWEV 63

RESULT 3  
MSPL\_PLAF3 MSPL\_PLAF3 STANDARD; PRT; 1682 AA.  
ID AC PI9598; Q25921;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS) (PMMA) (P190).  
DN DE MSP-1.  
GS Plasmodium falciparum (isolate ro-33 / Ghana).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5834;  
RN [1]  
RX MEDLINE=88166657; PubMed=3327688;  
RA Certa U., Rotmann D., Matile H., Reber-Liske R.;  
RT "A naturally occurring gene encoding the major surface antigen precursor p190 of Plasmodium falciparum lacks tripeptide repeats." J. EMBO J. 6:4137-4142(1987).  
RL [2]  
RN SEQUENCE OF 1032-1682 FROM N.A.  
RX MEDLINE=95354793; PubMed=7628566;  
RA Tolle R., Buiard H., Cooper J.A.

Query Match 100.0%; Score 74; DB 1; Length 1314;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;

RT \*Plasmodium falciparum: variations within the C-terminal region of  
RL merozoite surface antigen-1.\*;  
RT Exp. Parasitol. 81:47-54(1995).  
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR  
CC (POTENTIAL).  
CC -!- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 42  
CC KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF  
CC MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.  
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CC -----  
DR EMBL; M35727; AAA29715.1; -;  
DR EMBL; Y00087; CAA68280.1; -;  
DR EMBL; Z35326; CAA84555.1; -;  
DR PIR; S06286; S06286.  
DR InterPro: IPR000561; EGF-like.  
DR Pfam: PF00008; EGF; 1.  
KW Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;  
KW Transmembrane; GPI-anchor.  
FT SIGNAL 1 19  
FT CHAIN 20 1682  
FT TRANSMEM 1666 1682  
FT CARBOHYD 233 233  
FT CARBOHYD 462 462  
FT CARBOHYD 528 528  
FT CARBOHYD 599 599  
FT CARBOHYD 785 785  
FT CARBOHYD 881 881  
FT CARBOHYD 901 901  
FT CARBOHYD 947 947  
FT CARBOHYD 1071 1071  
FT CARBOHYD 1178 1178  
FT CARBOHYD 1569 1569  
SQ SEQUENCE 1682 AA; 192462 MW; C82A1E159948CAD6 CRC64;  
  
Query Match 57.4%; Score 42.5; DB 1; Length 1682;  
Best Local Similarity 60.0%; Pred. No. 11;  
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;  
  
QY 1 QVIKANSKFI-GITE 14  
Db 983 QFVKSNSKVTGLTE 997  
|:::||||| |::|  
  
RESULT 4  
MSPL\_PLAFF STANDARD; PRT; 1701 AA.  
AC P13819;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)  
DE (PMMSA).  
GN MSP-1.  
OS Plasmodium falciparum (isolate FC27 / Papua New Guinea).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5837;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88142999; PubMed=2449612;  
RA Peterson M.G., Coppel R.L., McIntyre P., Langford C.J., Woodrow G.,  
RA Brown G.V., Anders R.F., Kemp D.J.;  
RT "Variation in the precursor to the major merozoite surface antigens  
RT of Plasmodium falciparum.";  
RL Mol. Biochem. Parasitol. 27:291-302(1988).  
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR

CC (POTENTIAL).  
CC -!- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 42  
CC KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF  
CC MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.  
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CC -----  
DR EMBL; M19143; AAA29653.1; -;  
DR PIR; A54498; A54498.  
DR InterPro: IPR000561; EGF-like.  
DR Pfam: PF00008; EGF; 1.  
KW Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;  
KW Transmembrane; GPI-anchor.  
FT SIGNAL 1 19  
FT CHAIN 20 1701  
FT CARBOHYD 110 110  
FT CARBOHYD 239 239  
FT CARBOHYD 470 470  
FT CARBOHYD 536 536  
FT CARBOHYD 607 607  
FT CARBOHYD 802 802  
FT CARBOHYD 899 899  
FT CARBOHYD 919 919  
FT CARBOHYD 965 965  
FT CARBOHYD 991 991  
FT CARBOHYD 1089 1089  
FT CARBOHYD 1196 1196  
FT CARBOHYD 1588 1588  
SQ SEQUENCE 1701 AA; 193719 MW; 3920B75E73D38552 CRC64;  
  
Query Match 57.4%; Score 42.5; DB 1; Length 1701;  
Best Local Similarity 60.0%; Pred. No. 11;  
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;  
  
QY 1 QVIKANSKFI-GITE 14  
Db 1001 QFVKSNSKVTGLTE 1015  
|:::||||| |::|  
  
RESULT 5  
MSPL\_PLAFF STANDARD; PRT; 1701 AA.  
AC P08569;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)  
DE (PMMSA) (P190).  
GN MSP-1.  
OS Plasmodium falciparum (isolate mad20 / Papua New Guinea).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=70153;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88011243; PubMed=3079521;  
RA Tanabe K., Mackay M., Goman M., Scaife J.G.;  
RT "Allelic dimorphism in a surface antigen gene of the malaria parasite  
RT Plasmodium falciparum.";  
RL J. Mol. Biol. 195:273-287(1987).  
RN [2]  
RP REVISIONS TO 1403; 1569 AND 1629.  
RA Tanabe K.;  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 1-115 FROM N.A.  
RX MEDLINE=86136024; PubMed=3004972;

RA Mackay M., Goman M., Bone N., Hyde J.E., Scaife J., Certa U.,  
 RA Stunnenberg H., Bujard H.;  
 RT "Polymorphism of the precursor for the major surface antigens of  
 RT Plasmodium falciparum merozoites: studies at the genetic level.";  
 RL EMBO J. 4:3823-3829(1985).  
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR  
 CC (POTENTIAL).  
 CC -1- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 42  
 CC KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF  
 CC MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.  
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 CC -----  
 DR EMBL; X05624; CAA29112.1; -  
 DR PIR; A26868; A26868.  
 DR PIR; B25120; B25120.  
 DR InterPro: IPR000561; EGF-like.  
 DR Pfam: PF00008; EGF; 1  
 DR Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;  
 KW Transmembrane; GPI-anchor.  
 KW SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 1701 MEROZOITE SURFACE PROTEIN 1.  
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 470 470 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 536 536 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 802 802 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 899 899 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 919 919 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 965 965 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 991 991 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1089 1089 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1196 1196 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1588 1588 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 1701 AA; 193768 MW; 3FC2EC59AF96EA98 CRC64;

Query Match 57.48; Score 42.5; DB 1; Length 1701;  
 Best Local Similarity 60.0%; Pred. No. 11;  
 Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Oy 1 QYIKANSKFI-GITE 14  
 I:::|||||I::I  
 Db 1001 QFVKSNSKVIITGLTE 1015

RESULT 6  
 MSPL\_PLAFC  
 ID MSPL\_PLAFC STANDARD; PRT; 1726 AA.  
 AC P04934;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)  
 DE (PMMSA) (P195).  
 GN MSP-1.  
 OS Plasmodium falciparum (isolate Camp / Malaysia).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5835;  
 RN [1]  
 RP SEQUENCE OF 1-1103 FROM N.A.  
 RX MEDLINE=86205236; PubMed=3517809;  
 RA Weber J.L., Leininger W.M., Lyon J.A.;  
 RT "Variation in the gene encoding a major merozoite surface antigen of  
 RT the human malaria parasite Plasmodium falciparum.";  
 RL Nucleic Acids Res. 14:3311-3323(1986).

RN SEQUENCE OF 1104-1726 FROM N.A.  
 RP MEDLINE=88143999; PubMed=3278296;  
 RX Weber J.L., Sim B.K.L., Lyon J.A., Wolff R.;  
 RT "Merozoite surface protein sequence from the Camp strain of the human  
 RT malaria parasite Plasmodium falciparum.";  
 RL Nucleic Acids Res. 16:1206-1206(1988).  
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR  
 CC (POTENTIAL).  
 CC -1- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 42  
 CC KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF  
 CC MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.  
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 CC -----  
 DR EMBL; X03831; CAA27446.1; -  
 DR PIR; A23386; SAZQCM.  
 DR InterPro: IPR000561; EGF-like.  
 DR Pfam: PF00008; EGF; 1  
 DR Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;  
 KW Transmembrane; GPI-anchor.  
 KW SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 1726 MEROZOITE SURFACE PROTEIN 1.  
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 272 272 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 501 501 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 567 567 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 638 638 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 827 827 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 924 924 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 944 944 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 990 990 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1016 1016 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1114 1114 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1221 1221 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1613 1613 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 1726 AA; 196197 MW; DD8AD45FA352BCF3 CRC64;

Query Match 57.48; Score 42.5; DB 1; Length 1726;  
 Best Local Similarity 60.0%; Pred. No. 11;  
 Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Oy 1 QYIKANSKFI-GITE 14  
 I:::|||||I::I  
 Db 1026 QFVKSNSKVIITGLTE 1040

RESULT 7  
 MSPL\_PLAFC  
 ID MSPL\_PLAFC STANDARD; PRT; 1726 AA.  
 AC P50455;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)  
 DE (PMMSA) (P195).  
 GN MSP-1.  
 OS Plasmodium falciparum (isolate Palo Alto / Uganda).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=57270;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89005525; PubMed=3049134;  
 RA Chang S.P., Kramer K.J., Yamaga K.M., Kato A., Case S.E.,  
 RA Siddiqui W.A.;  
 RT "Plasmodium falciparum: gene structure and hydropathy profile of the

RT major merozoite surface antigen (gp195) of the Uganda-Palo Alto  
RT isolate.";  
RL Exp. Parasitol. 67:1-11(1988).  
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR  
CC (POTENTIAL).  
CC  
CC -1- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 42  
CC KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF  
CC MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.  
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CC  
DR EMBL; M37213; AAA29611.1; -  
DR InterPro; IPR000561; EGF-like.  
DR Pfam; PF00008; EGF; 1.  
KW Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;  
KW Transmembrane; GPI-anchor.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 1726 MEROZOITE SURFACE PROTEIN 1.  
FT CARBOHYD 133 133 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 272 272 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 501 501 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 567 567 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 638 638 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 827 827 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 924 924 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 944 944 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 990 990 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 1016 1016 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 1114 1114 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 1221 1221 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 1613 1613 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT SEQUENCE 1726 AA; 196174 MW; 5B59CEEFA2F9A026 CRC64;  
SQ  
  
Query Match 57.4%; Score 42.5; DB 1; Length 1726;  
Best Local Similarity 60.0%; Pred. No. 11;  
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;  
  
QY 1 QVVKANSKFI-GITE 14  
DB 1026 QVVKNSKVITGLTE 1040  
I:::|::| |::|  
  
RESULT 8  
PYRC\_SERMA STANDARD; PRT; 204 AA.  
AC Q9S3S1;  
DT 20-AUG-2001 (Rel. 40, Created)  
DT 20-AUG-2001 (Rel. 40, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE DIHYDROOROTASE (EC 3.5.2.3) (DHIOASE) (FRAGMENT).  
GN PYRC.  
OS Serratia marcescens.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Serratia.  
OX NCBI\_TaxID=615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SM6;  
RA Berkmen M., Benedik M.J.;  
RT "Dini inhibits transcription of Serratia marcescens nuclease.";  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: DIHYDROOROTATE + H(2)O = N-CARBAMOYL-  
CC L-ASPARTATE.  
CC  
CC -1- COFACTOR: THIS ENZYME TIGHTLY BINDS ONE ZINC ATOM PER CHAIN WHICH  
CC IS REQUIRED FOR THE CATALYTIC MECHANISM. IT ALSO BINDS WEAKLY TO  
CC TWO OTHERS ZINCS WHICH ARE NOT ESSENTIAL FOR ACTIVITY (BY

CC SIMILARITY).  
CC -1- PATHWAY: THIRD STEP IN PYRIMIDINE BIOSYNTHESIS.  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE DHIOASE FAMILY. SUBFAMILY 1.  
CC  
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CC  
DR EMBL; AP175466; AAD50307.1; ALT INIT.  
DR InterPro; IPR002195; Dihydroorotase.  
DR PROSITE; PS00482; DIHYDROOROTASE\_1; PARTIAL.  
DR PROSITE; PS00483; DIHYDROOROTASE\_2; 1.  
KW Pyrimidine biosynthesis; Hydrolase; Zinc.  
FT NON\_TER 1  
FT SEQUENCE 204 AA; 22899 MW; 9DB0B6C9B834B310 CRC64;  
SQ  
  
Query Match 55.4%; Score 41; DB 1; Length 204;  
Best Local Similarity 46.2%; Pred. No. 2.3;  
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 QYIKANSKFIGIT 13  
DB 42 QYVQAGNRFLGAT 54  
I:::|::| |::|  
  
RESULT 9  
V120\_HSVSA STANDARD; PRT; 899 AA.  
ID V120\_HSVSA  
AC Q01055;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE CAPSID ASSEMBLY PROTEIN 63.  
GN 63 OR PERFL.  
OS Herpesvirus saimiri (strain 11).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Gammaherpesvirinae; Rhadinovirus.  
OX NCBI\_TaxID=10383;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92333688; PubMed=1321287;  
RA Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Blesinger B.,  
RA Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,  
RA Honess R.W.;  
RT "Primary structure of the herpesvirus saimiri genome.";  
RL J. Virol. 66:5047-5058(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92330228; PubMed=1314457;  
RA Nicholas J., Cameron K.R., Coleman H., Newman C., Honess R.W.;  
RT "Analysis of nucleotide sequence of the rightmost 43 kbp of  
RT herpesvirus saimiri (HVS) L-DNA: general conservation of genetic  
RT organization between HVS and Epstein-Barr virus.";  
RL Virology 188:296-310(1992).  
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL37,  
CC EBV-1 23, EBV BOLFI, VZV 21, HVS-1 63, AND HCMV UL47.  
CC  
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CC  
DR EMBL; X64346; CAA45686.1; -  
DR EMBL; M86409; AAA46139.1; -

```

Query Match          54.1%; Score 40; DB 1; Length 194;
Best Local Similarity 53.3%; Pred. No. 3.3;
Matches      8; Conservative      4; Mismatches      3; Indels      0; Gaps      0;

1 QYKANSKFGITEL 15
  11: 11111:
147 QYMKSLGFGITDV 161

RESULT 11
PEPTID_LACLC
PEPTID_LACLC STANDARD; PRT; 601 AA.
P54124; P94880;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
OLIGONDOPEPTIDASE F, PLASMID (EC 3.4.24.-).
PEPFI OR PEPF.
Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
Plasmid pLP763.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
Lactococcus
NCBI_TaxID=1359;
[1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=NCDO 763;
MEDLINE=95096044; PubMed=7798200;
Monnet V., Nardi M., Chopin A., Chopin M.-C., Gripon J.-C.;
"Biochemical and genetic characterization of PepF, an oligopeptidase
from Lactococcus lactis.";
J. Biol. Chem. 269:32070-32076(1994).
[2]
SEQUENCE FROM N.A.
STRAIN=NCDO 763;
MEDLINE=97352670; PubMed=9209029;
Nardi M., Renault P., Monnet V.;
"Duplication of the pepf gene and shuffling of DNA fragments on the
lactose plasmid of Lactococcus lactis.";
J. Bacteriol. 179:4164-4171(1997).
-1- FUNCTION: HYDROLYSES PEPTIDES CONTAINING BETWEEN 7 AND 17 AMINO
ACIDS WITH A RATHER WIDE SPECIFICITY.
-1- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3 (ZINC METALLOPROTEASE);
ALSO KNOWN AS THE THIMET OLIGOPEPTIDASE SUBFAMILY.
-----
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-----
EMBL; J25222; CAA83534.1; -
EMBL; X99798; CAA68133.1; -
MEROPS; M03.007; -
InterPro; IPR001567; Peptidase_M3.
InterPro; IPR000130; Zn_MTPeptidse.
Pfam; PF01432; Peptidase_M3; 1.
PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
Hydrolase; Metalloprotease; zinc; Plasmid.
METAL 387 387 ZINC (CATALYTIC) (BY SIMILARITY).
ACT_SITE 388 388 ZINC (CATALYTIC) (BY SIMILARITY).
METAL 391 391 ZINC (CATALYTIC) (BY SIMILARITY).
METAL 394 394 ZINC (CATALYTIC) (BY SIMILARITY).
CONFLICT 518 518 F -> S (IN REF. 2).
SEQUENCE 601 AA; 69674 MW; C8B5C519FFA2F787 CRC64;

Query Match          54.1%; Score 40; DB 1; Length 601;
Best Local Similarity 46.7%; Pred. No. 11;
Matches      4; Indels      0; Gaps      0;

```

QY 1 QYIKANSKFIGITEL 15  
DB 284 RYIELRKKILGITDL 298

RESULT 12  
YHJ9\_YEAST

ID YHJ9\_YEAST STANDARD; PRT; 644 AA.  
AC P38694;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN IN FILI-VMA10  
DE INTERGENIC REGION.  
GN YHR039C.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;

-----  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S288C / AB972;  
RX MEDLINE=94378003; PubMed=8091229;  
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,  
Du Z., Favella A., Fulton L., Gattung S., Geisel C., Kirsten J.,  
Kucaba T., Hillier L., Jler M., Johnston L., Langston Y.,  
Latreille P., Louis E.J., Macri C., Mardis E., Meneses S., Mouser L.,  
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,  
Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,  
Vaudin M.;  
RA "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome  
VIII.";  
RT Science 265:2077-2082(1994).  
RL  
CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.  
-----  
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-----  
CC

DR EMBL; U00062; AAB68915.1; -  
DR PIR; S46746; S46746.  
DR SGD; S0001081; YHR039C.

DR InterPro: IPR002086; Aldehyde\_dehydr.  
DR Pfam; PF00171; aldedh; 1.  
DR PROSITE; PS00070; ALDEHYDE-DEHYDR\_CYS; 1.  
DR PROSITE; PS00687; ALDEHYDE-DEHYDR\_GLU; 1.  
KW Hypothetical protein; Oxidoreductase.  
FT ACT\_SITE 354 354 BY SIMILARITY.  
FT ACT\_SITE 389 389 BY SIMILARITY.  
SQ SEQUENCE 644 AA; 71320 MW; 54DADDAEB2A16D4D CRC64;

Query Match 54.1%; Score 40; DB 1; Length 644;  
Best Local Similarity 60.0%; Pred. No. 12;  
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15  
DB 38 QIIQDNQKLIGITTL 52

RESULT 13  
KAD\_MYCCA

ID KAD\_MYCCA STANDARD; PRT; 213 AA.  
AC P10251;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE ADENYLATE KINASE (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE).

GN ADK.  
OS Mycoplasma capricolum.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;  
OC Entomoplasmataceae.  
OX NCBI\_TaxID=2095;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 27343 / KID;  
RX MEDLINE=88142549; PubMed=3481422;  
RA Ohkubo S., Muto A., Kawauchi Y., Yamao F., Osawa S.;  
RT "The ribosomal protein gene cluster of Mycoplasma capricolum.";  
RL Mol. Gen. Genet. 210:314-322(1987).  
CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR  
CC MAINTENANCE AND CELL GROWTH.

CC -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.  
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.

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CC

DR EMBL; X06414; CAA29724.1; -  
DR PIR; S02851; KIYMC.  
DR HSSP; P27142; LZIO.

DR InterPro: IPR000850; Adenylate\_kin.  
DR Pfam; PF00406; adenylatekinase; 1.  
DR PRINTS; PR00094; ADENYLTKINASE.  
DR PRODOM; PD000657; Adenylate\_kin; 1.  
DR PROSITE; PS00113; ADENYLATE\_KINASE; 1.  
KW Transferase; Kinase; ATP-binding.  
FT NP\_BIND 7 15 ATP (BY SIMILARITY).  
SQ SEQUENCE 213 AA; 24616 MW; FBCFA426B6F92E16 CRC64;

Query Match 52.7%; Score 39; DB 1; Length 213;  
Best Local Similarity 72.7%; Pred. No. 5.6;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YIKANSKFIGI 12  
DB 183 YFRTNSKFIEI 193

RESULT 14  
YD83\_METJA

ID YD83\_METJA STANDARD; PRT; 256 AA.  
AC Q58778;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE HYPOTHETICAL PROTEIN MJ1383 PRECURSOR.  
GN MJ1383.  
OS Methanococcus jannaschii.  
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;  
OC Methanococcus.  
OX NCBI\_TaxID=2190;  
RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;  
RX MEDLINE=96337999; PubMed=8688087;  
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,  
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,  
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,  
Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,  
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

```
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RL jannaschii.";
RL Science 273:11058-1073(1996).
CC -!- SIMILARITY: TO M.JANNASCHII MJ0761.
CC -----
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CC -----
DR EMBL; U67578; AAB99393.1; -
DR TIGR; MJ1383; -
DR InterPro; IPR001130; UPF00006.
DR Pfam; PF01026; TatD.DNase; 1.
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 256 HYPOTHETICAL.PROTEIN MJ1383.
SQ SEQUENCE 256 AA; 29036 MW; 6D26F427EAB54675 CRC64;

Query Match 51.4%; Score 38; DB 1; Length 256;
Best Local Similarity 50.0%; Pred. No. 10;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 YKANSKFIGITEL 15
II II: :|| I;
DB 89 YINYSRVVGIGEI 102

RESULT 15
TRUB_AQUAE
ID TRUB_AQUAE STANDARD; PRT; 287 AA.
AC O66922;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55
DE SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL
DE HYDROLYASE).
DE GN TRUB OR AQ.705.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aufay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RL Nature 392:353-358(1998).
CC -!- FUNCTION: FORMATION OF PSEUDOURIDINE AT POSITION 55 IN THE
CC PSI GC LOOP OF TRANSFER RNAS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: URACIL + D-RIBOSE 5-PHOSPHATE = PSEUDOURIDINE
CC 5'-PHOSPHATE + H(2)O.
CC -!- SIMILARITY: BELONGS TO THE TRUB FAMILY OF PSEUDOURIDINE SYNTHASES.
CC -----
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CC -----
DR EMBL; AE000703; AAC06885.1; -
DR InterPro; IPR002501; Trub_N.
```

```
DR Pfam; PF01509; Trub_N; 1.
KW Lyase; tRNA processing; Complete proteome.
SQ SEQUENCE 287 AA; 32259 MW; 2E58C1B7CEAD58AA CRC64;
```

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Query Match 51.4%; Score 38; DB 1; Length 287;
Best Local Similarity 69.2%; Pred. No. 12;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 IKANSKFIGITEL 15
II :||||| II
DB 263 IYDSKFIGIGEL 275
```

Search completed: January 29, 2002, 11:16:20  
Job time: 149 sec



GenCore version 4.5  
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OH protein - protein search, using sw model

Run on: January 29, 2002, 11:15:53 ; Search time 62.77 Seconds  
(without alignments)  
51.266 Million cell updates/sec

Title: US-09-763-397a-25  
Perfect score: 108  
Sequence: 1 MKFLVNVALVFVWYISYIYAD 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP-archaea:\*  
2: SP-bacteria:\*  
3: SP-fungi:\*  
4: SP-human:\*  
5: SP-invertebrate:\*  
6: SP-mammal:\*  
7: SP-mhc:\*  
8: SP-organella:\*  
9: SP-phage:\*  
10: SP-plant:\*  
11: SP-rodent:\*  
12: SP-virus:\*  
13: SP-vertebrate:\*  
14: SP-unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	50.9	205	2	09XD01
2	54	50.0	205	2	09XD00
3	52	48.1	209	2	046325
4	52	43.1	209	2	09S4S8
5	52	48.1	209	2	09R416
6	50.5	46.8	352	2	09CG28
7	49	45.4	669	5	09VPG2
8	48	44.4	40	8	034216
9	47	43.5	65	2	099TK2
10	47	43.5	157	13	098882
11	47	43.5	162	13	091AK7
12	47	43.5	162	13	091AK6
13	47	43.5	162	13	091AK5
14	46	42.6	940	13	073635
15	45	41.7	137	11	09JK21
16	45	41.7	320	5	09XU6
17	45	41.7	331	12	09YK45
18	45	41.7	379	2	087181
19	45	41.7	425	5	019125

20	45	41.7	446	2	09S115	09s115 streptococ
21	45	41.7	506	5	021420	021420 caenorhabd
22	45	41.7	681	5	09VE33	09ve33 drosophila
23	45	41.7	1260	5	09XZC5	09xzcs cryptospori
24	44.5	41.2	210	8	09G8P4	09g8p4 naegleria g
25	44	40.7	222	13	P70023	P70023 xenopus lae
26	44	40.7	321	11	09QXFS	09qxf5 mesocricetu
27	44	40.7	373	5	021149	021149 caenorhabd
28	44	40.7	377	2	034161	034161 salmone
29	44	40.7	492	5	027505	027505 caenorhabd
30	44	40.7	495	2	09X4D3	09x4d3 streptococ
31	44	40.7	580	5	016920	016920 caenorhabd
32	44	40.7	687	9	09MC93	09mc93 bacterioph
33	43.5	40.3	576	3	09Y7S4	09y7s4 schizosacch
34	43.5	40.3	580	3	059698	059698 schizosacch
35	43	39.8	94	10	09LYP8	09lyp8 arabidopsis
36	43	39.8	217	5	017717	017717 caenorhabd
37	43	39.8	254	2	09LBY3	09lby3 shewanella
38	43	39.8	269	10	039647	039647 cucurbita m
39	43	39.8	300	2	09K112	09k112 vibrio chol
40	43	39.8	338	5	045300	045300 caenorhabd
41	43	39.8	372	3	042944	042944 schizosacch
42	43	39.8	379	13	09DG05	09dg05 gallus gall
43	43	39.8	424	13	09DG06	09dg06 gallus gall
44	43	39.8	442	1	058688	058688 pyrococcus
45	43	39.8	442	2	09HTR7	09htr7 pseudomonas

## ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	205 AA.
ID 09XD01			
AC 09XD01			
DT 01-NOV-1999 (TREMBlrel. 12, Created)			
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)			
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)			
DE MAJOR ANTIGENIC PROTEIN 2 HOMOLOG.			
OS Ehrlichia canis.			
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;			
OC Rickettsiaceae; Ehrlichiae; Ehrlichia.			
OX NCBI_Taxid=944;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=OKLAHOMA;			
RA Bowie M.V., Reddy G.R., Semu S.M., Mahan S.M., Barbet A.F.;			
RT "Potential Value of Major Antigenic Protein 2 for serological			
RT Diagnosis of Heartwater and Related Ehrlichial Infections.";			
RL Clin. Diagn. Lab. Immunol. 0:0-0(1999).			
DR EMBL: AF117730; AAD40619.1; -;			
DR InterPro: IPR003782; SCOL_Senc.			
DR Pfam: PF02630; SCOL_Senc: 1.			
SQ SEQUENCE 205 AA: 23169 MW: 756B50A3304C13CB CRC64;			
Query Match	50.9%	Score 55:	DB 2: Length 205:
Best Local Similarity	40.0%	Pred. No. 3.4;	
Matches 8; Conservative	7;	Mismatches 5;	Indels 0;
DB 4 MKFLVNVALVFVWYISYIY 20			
QY : :: : : : : : : : :			
DB 4 IKFLVNVCLLFAITFLCY 23			
QY : : : : : : : : :			
RESULT 2	PRELIMINARY:	PRT:	205 AA.
ID 09XD00			
AC 09XD00			
DT 01-NOV-1999 (TREMBlrel. 12, Created)			
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)			
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)			
DE MAJOR ANTIGENIC PROTEIN 2 HOMOLOG.			

OS *Enrichella chaffeensis*.  
OC Bacteria: Proteobacteria: alpha subdivision: Rickettsiales;  
OC Rickettsiaceae: Ehrlichiae, Ehrlichia.  
OX NCBI\_TaxID=945;  
[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=ARKANSAS;  
RC Boyle M.V., Reddy G.R., Semu S.M., Mahan S.M., Barbet A.F.;  
RA "Potential Value of Major Antigenic Protein 2 for Serological  
RT Diagnosis of Heartwater and Related Ehrlichial Infections.";  
RL Clin. Diagn. Lab. Immunol. 0:0-0(1999).  
DR EMBL: AF117731; AAD40620.1; -  
DR InterPro: IPR003783; SCOL:SENC.  
DR Pfam: PF02630; SCOL:SENC.1.  
ER  
SQ SEQUENCE 205 AA; 23142 MW; 561DC264B6EC9736 CR664;

Query Match	50.0%;	Score 54;	DB 2;	Length 205;
Best Local Similarity	35.0%;	Pred. No. 4.6;		
Matches	?	Conservative <sup>1</sup> 8;	Mismatches 5;	Indels 0;
			Gaps	0;

```
QY 1 MKFLVNAALVEMVVYISYIY 20
    :|:|:|. |:| ::| |
Db 4 IKFILNICLLFAAIFLGSY 23
```

RESULT	3			
ID	046325	PRELIMINARY;	PRT;	209 AA.
AC	046325;			
DT	01-NOV-1996 (TReMBLrel. 01, Created)			
DT	01-NOV-1996 (TReMBLrel. 01, last sequence update)			
DT	01-JUN-2001 (TReMBLrel. 17, last annotation update)			
DE	IMMUNODOMINANT PROTEIN PRECURSOR.			
OS	Cowdria ruminantium.			
OC	Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;			
OC	Rickettsiaceae; Ehrlichieae; Cowdria.			
OX	NCBI_TaxID=779;			
RN	11)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95005467; PubMed=7921263;			
RA	Mahan S.M., McGuire T.C., Semu S.M., Bowle M.V., Jongejan F.,			
RA	Rurangitwa F.R., Barbet A.F.;			
RT	"Molecular cloning of a gene encoding the immunogenic 21 kDa protein			
RT	of Cowdria ruminantium."			
RL	Microbiology 140:2135-2142(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=HIGHWAY;			
RA	Bowle M.V., Reddy G.R., Semu S.M., Barbet A.F.;			
RT	Potential Value of Major Antigenic Protein 2 for Serological			
RT	Diagnosis of Heartwater and Related Ehrlichial Infections."			
RL	Clin. Diagn. Lab. Immunol. 0:0-0(1999).			
DR	EMBL; AF17385; AAA50280.1; "			
DR	EMBL; AF17727; AAD40616.1; "			
DR	InterPro: IPR003782; SCOP_Senc.			
DR	Pfam: PF02630; SCOP_Senc; 1.			
DR	Signal.			
FT	STGNAL.	1	19	POTENTIAL.
FT	CHAIN	20	209	IMMUNODOMINANT PROTEIN.
SQ	SEQUENCE	209 AA;	2360 MW;	43D107A87F0B9345 CR64;

Query Match	48.1%;	Score 52;	DB 2;	Length 209;
Best Local Similarity	35.0%;	Pred. No. 8.7;		
Matches	7; Conservative	8; Mismatches	5; Indels	0; Gaps

```
QY 1 MKFLVWALVFMVYISYIY 20
      :|:|:|:|:|:|:|:|:|
Db 8 IKFILNCLLEFA:IFLGYSY 27
```

## RESULT 4

ID	Q9S4S8	PRELIMINARY;	PTI;	209 AA.
AC	Q9S4S8:			
DT	01-MAY-2000 (TREMBLrel_13,	Created		
DT	01-MAY-2000 (TREMBLrel_13,	Last sequence update)		
DT	01-JUN-2001 (TREMBLrel_17,	Last annotation update)		
DE	MAJOR ANTIGENIC PROTEIN 2.			
OS	Cowdria ruminantium.			
OC	Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;			
OC	Rickettsiaceae; Ehrlichiaeae; Cowdria.			
OX	NCBI_TaxID=779;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	BOWLEIN-ANTIGUA;			
RA	Bowle M.V., Reddy G.R., Semu S.M., Mahan S.M., Barbet A.F.;			
RT	"Potential Value of Major Antigenic Protein 2 for Serological			
RT	Diagnosis of Heartwater and Related Ehrlichial Infections.";			
RL	Clin. Diagn. Lab. Immunol. 0:0-0(1999).			
DR	EMBL: AF117726; AIMP0615.1; "			
DR	Interpro: IPR003782; SCOL_Senc.			
DR	Pfam: PF02630; SCOL_Senc.1			
SQ	SEQUENCE	209 AA;	23S04 MW;	8FF9A535E1737569 CRC64;

Query Match	48.18;	Score 52;	DB 2;	Length 209;
Best Local Similarity	35.08;	Pred. No. 8.7;		
Matches	7;	Conservative	8;	Mismatches 5;
				Indels 0;
				Gaps 0;

```
QY 1 MKFLVNVALVEMVVYISYIX 20
    :||::|:|:|::|:|
Db 8 IKFILNCLLFAAIFLGYSY 27
```

ID	Accession	Label	Created	Updated	Sequence	Annotations
09R416	09R416	PRELIMINARY;		209 AA.		
AC	09R416					
AD	01-MAY-2000	(TREMblrel, 13,	Created			
DE	01-MAY-2000	(TREMblrel, 13,	Last sequence update)			
DT	01-JUN-2001	(TREMblrel, 11,	Last annotation update)			
DE	MAJOR ANTIGENIC PROTEIN 2.					
OS	Coccidia tumidulum.					
OC	Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;					
OC	Rickettsiaceae; Ehrlichiae; Cowdria.					
OX	NCBI_TaxID=779;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN-UM BAINEM, AND PALM RIVER;					
RA	Bowie M.V., Reddy G.R., Semu S.M., Mahan S.M., Barbett A.F.;					
RT	Potential Value of Major Antigenic Protein 2 for Serological					
RT	Diagnosis of Heartwater and Related Ehrlichial Infections.;					
RL	Clin. Diagn. Lab. Immunol. 0:0-0(1999).					
DR	EMBL: AF117729; AAA0618.1; -					
DR	EMBL: AF117728; AAA0617.1; -					
DR	InterPro: IPR003782; SCOL_Senc.					
DR	Plan: PF02630; SCOL_Senc; 1;					
SQ	SEQUENCE 209 AA; 23562 MW;					

Query Match	48.1%;	Score 52;	DB 2;	Length 209;
Best Local Similarity	35.0%;	Pred. No. 8.7;		
Matches	7;	Conservative	8;	Mismatches 5;
				Indels 0;
				Gaps 0;

QY	1 MKFLVNAVLEVMVVYSIY	20
	: :: : : :: :	
Db	8 IKFILNCLLFAAIFLGYSY	27

RESULT	6	
Q9CGZ8		
ID	Q9CGZ8	PRELIMINARY;
AC	Q9CGZ8;	PRT; 352 AA
DT	01-JUN-2001	(Tremblere, 17, Created)

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclelj J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Pui W., Reese M.G.,  
RA Rehnet K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Klamos I., Stimpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E.C., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang K., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
DR EMBL: AE003591; AAF51591.1; -  
DR FlyBase: FBgn0036984; CG3248.  
DR InterPro: IPR002293; AA:tel\_permease-1.  
DR InterPro: IPR002297; AA:amino\_acid\_permease.  
DR Pfam: PF00324; aa\_permeases; 1.  
XQ SEQUENCE 669 AA: 71856 MW: 02207F48F5569053 CRC64:

	Query Match	45.4%;	Score 49;	DB 5;	Length 669;
	Best Local Similarity	42.1%;	Pred. No. 60;		
	Matches	8; Conservative	7; Mismatches	4; Indels	0; Gaps
Oy	LVNVALVPMVVYISITPAD	22	.		
	:   :	:   :			-
b	LVNIAVMVLVISGFMWAD	220			
	Vdb				

[illegible]

01-JUN-2001 (TRENBLER, 17, last annotation update)  
 HYPOTHETICAL PROTEIN SA1477.  
 SA1477  
 OS Staphylococcus aureus subsp. aureus N315.  
 OC Bacillus/Staphylococcus group; Staphylococcus.  
 DE Bacillus/Staphylococcus group; Staphylococcus.  
 NCBI\_TaxID=158679;  
 [1]  
 RP  
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,  
 Cui L., Oguchi A., Aoki K.I., Nagai Y., Ito T., Kanamori M.,  
 Takamatsu H., Maruyama A., Murakami H., Hoshiyama A., Mizutani-Oi Y.,  
 Takamashi N.K., Sawano T., Inoue R.I., Kato C., Sekimizu K.,  
 Yamashita H., Kohda S., Goto S., Takai O., Kashiwa M.,  
 Ogasawara N., Hayashi H., Hiratake K., Shiba T., Hattori M.,  
 "Whole genome sequencing of methicillin-resistant Staphylococcus  
 aureus.";  
 RT Lancet 357:1225-1240(2001).  
 DR EMBL: AP003134; BAB42743.1;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 65 AA; 7317 MW; D875C82A08C7058 CRC64;

Query Match 43.5%; Score 47; DB 13; Length 65;  
 Best Local Similarity 38.9%; Pred. No. 15;  
 Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;  
 OY 1 MWLVNVALVPMVYISY 18  
 DB 24 LRLTLFLLILISYV 41

RESULT 10  
 ID O98882; PRELIMINARY; PRT; 157 AA.  
 AC O98882;  
 DT 01-FEB-1997 (TRENBLER, 02, Created)  
 DT 01-FEB-1997 (TRENBLER, 02, Last sequence update)  
 DT 01-JUN-2001 (TRENBLER, 17, Last annotation update)  
 DE ODOURANT RECEPTOR 1 (FRAGMENT).  
 GN ZORI  
 OS Brachydanio rerio (zebrafish) (zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.  
 NCBI\_TaxID=7955;  
 RN [1]  
 RP  
 RA "SEQUENCE FROM N.A.  
 RX MEDLINE-97075163; PubMed-8917589;  
 RA Weich F., Nadler W., Korsching S.  
 RT "Nested expression domains for odorant receptors in zebrafish  
 olfactory epithelium.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 93:13321-13326(1996).  
 DR EMBL: U72683; AAB38866.1;  
 DR ZFIN: ZDB-GENE-990415-190; zotl.  
 DR InterPro: IPR000276; GPCR\_Rhodopsin.  
 DR Pfam: PF00001; 2tm\_1; 1.  
 DR EMBL: AF198444; S6410.1; 97:2670-2674(2000).  
 DR InterPro: IPR000276; GPCR\_Rhodopsin.  
 DR Pfam: PF00001; 2tm\_1; 1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECPT\_FL\_2; 1.  
 KW Receptor.  
 FT NON\_TER 157  
 FT NON\_TER 157  
 SQ SEQUENCE 157 AA; 17656 MW; CE5738C349526C4 CRC64;

Query Match 43.5%; Score 47; DB 13; Length 157;  
 Best Local Similarity 41.2%; Pred. No. 32;  
 Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
 OY 4 LNVNVALVPMVYISY 20  
 DB 77 LRLTLFLLILISYV 93

RESULT 11  
 ID O91AK7; PRELIMINARY; PRT; 162 AA.  
 AC O91AK7;  
 DT 01-OCT-2000 (TRENBLER, 15, Created)  
 DT 01-OCT-2000 (TRENBLER, 15, Last sequence update)  
 DT 01-JUN-2001 (TRENBLER, 17, Last annotation update)  
 DE OLFACTORY RECEPTOR (FRAGMENT).  
 GN DREL  
 OS Brachydanio rerio (zebrafish) (zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.  
 NCBI\_TaxID=7955;  
 RN [1]  
 RP  
 RA "SEQUENCE FROM N.A.  
 RX MEDLINE-20183981; PubMed-10706615;  
 RA Rouquier S., Blancher A., Giorgi D.;  
 RT "The olfactory receptor gene repertoire in primates and mouse:  
 Evidence for reduction of the functional fraction in primates.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).  
 DR EMBL: AF198444; AAF40409.1;  
 DR InterPro: IPR000276; GPCR\_Rhodopsin.  
 DR Pfam: PF00001; 2tm\_1; 1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECPT\_FL\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1  
 FT NON\_TER 162  
 SQ SEQUENCE 162 AA; 18156 MW; FA77B0A46EFCB7A9 CRC64;

Query Match 43.5%; Score 47; DB 13; Length 162;  
 Best Local Similarity 41.2%; Pred. No. 33;  
 Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
 OY 4 LNVNVALVPMVYISY 20  
 DB 81 LRLTLFLLILISYV 97

RESULT 12  
 ID O91AK6; PRELIMINARY; PRT; 162 AA.  
 AC O91AK6;  
 DT 01-OCT-2000 (TRENBLER, 15, Created)  
 DT 01-OCT-2000 (TRENBLER, 15, Last sequence update)  
 DT 01-JUN-2001 (TRENBLER, 17, Last annotation update)  
 DE OLFACTORY RECEPTOR (FRAGMENT).  
 GN DREL  
 OS Brachydanio rerio (zebrafish) (zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.  
 NCBI\_TaxID=7955;  
 RN [1]  
 RP  
 RA "SEQUENCE FROM N.A.  
 RX MEDLINE-20183981; PubMed-10706615;  
 RA Rouquier S., Blancher A., Giorgi D.;  
 RT "The olfactory receptor gene repertoire in primates and mouse:  
 Evidence for reduction of the functional fraction in primates.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).  
 DR EMBL: AF198444; S6410.1; 97:2670-2674(2000).  
 DR InterPro: IPR000276; GPCR\_Rhodopsin.  
 DR Pfam: PF00001; 2tm\_1; 1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECPT\_FL\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1  
 FT NON\_TER 162  
 SQ SEQUENCE 162 AA; 18122 MW; 7877B0A46EFCB7A9 CRC64;

Query Match 43.5%; Score 47; DB 13; Length 162;  
 Best Local Similarity 41.2%; Pred. No. 33;  
 Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;



Mon Feb 4 15:23:47 2002

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